

```

1  GTCTTCCACCATGCACTCGCTGGGCTTCTCTGTGTGGCGTGTCTCTGCTCGCCGCTG
   +-----+-----+-----+-----+-----+-----+
60  CAGGAAGGTGTACGTAGCGACCCGGAAGAAGAGACACCCGACACAAGAGACGAGCGCGAC
   M H S L G F F S V A C S L L A A A -
   +-----+-----+-----+-----+-----+-----+
61  CGCTGCTCCCGGGTCTCGCGAGGCGCGCGCGCGCGCGCTTCGAGTCCGGACTCG
   +-----+-----+-----+-----+-----+-----+
   GCGACGAGGGCCAGGAGCGCTCCGCGGGCGCGCGCGCGGAAGCTCAGGCCCTGAGC
   L L P G P R E A P A A A A F E S G L D -
   +-----+-----+-----+-----+-----+-----+
121 ACCTCTCGGACGGGAGCCCGACGCGGGCGAGGCCACGGCTTATGCAAGCAAAGATCTGG
   +-----+-----+-----+-----+-----+-----+
   TGGAGAGCCCTGCGGCTCGGGCTGCGCCCGCTCCGGTGCCGAATACGTTTCGTCTAGACC
   L S D A E P D A G E A T A Y A S K D L E -
   +-----+-----+-----+-----+-----+-----+
181 AGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAACCTCATGACTGTACTCTACCCAGAAT
   +-----+-----+-----+-----+-----+-----+
   TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGGTCTTA
   E Q L R S V S S V D E L M T V L Y P E Y -
   +-----+-----+-----+-----+-----+-----+
241 ATTGGAAAATGTACAAGTGTCAAGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGG
   +-----+-----+-----+-----+-----+-----+
   TAACCTTTTACATGTTACAGATCGATTCCTTCCCGACCGTTGTATTGTCTCTGTGCC
   W K M Y K C Q L R K G G W Q H N R E Q A -
   +-----+-----+-----+-----+-----+-----+
300 CCAACCTCAACTCAAGGACAGAGAGACTATAAAATTGCTGCAGCACATTATAATACAG

```

MATCH WITH FIG. 1B

FIG. 1A

MATCH WITH FIG. 1A

301
GGTTGGAGTTGAGTTCCTGTCTTCTCTGTATATTTAAACGACGTCGTGTAATATATGTC
N L N S R T E E T I K F A A A H Y N T E -
360
AGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT
361
TCTAGAACTTTTCATAACTATTAATCACTCTTTCTGAGTTACGTACGGTGCCCTCCACA
I L K S I D N E W R K T Q C M P R E V C -
420
GTATAGATGTGGGAAGGAGTTTGGAGTCGCGACAACACCTTCTTTAAACCTCCATGTG
421
CATATCTACACCCCTTCCTCAAACCTCAGCGCTGTGTGTGGAAGAAATTTGGAGGTACAC
I D V G K E F G V A T N T F F K P P C V -
480
TGTCGGTCTACAGATGTGGGGGTGTCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA
481
ACAGGCAGATGTCTACACCCCCAACGACGTTATCACTCCCGACGTCACGTACTGTGGT
S V Y R C G G C C N S E G L Q C M N T S -
540
GCACGAGTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCCTCTCTCAAGGCCCA
541
CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTACGGAGAGAGAGTTCGGGGT
T S Y L S K T L F E I T V P L S Q G P K -
600
AACCAGTAACAATCAGTTTTCGCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG
601
TTGGTCATTGTTAGTCAAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTGACCTAC
P V T I S F A N H T S C R C M S K L D V -

MATCH WITH FIG. 1C

FIG. 1B

MATCH WITH FIG. 1B

661 TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACTACCACAGTGTC
 -----+-----+-----+-----+-----+-----+-----+
 AAATGTCTGTTCAGTAAGGTAATAATCTGCAAGGACGGTCGTTGTGATGGTGCACAG
 Y R Q V H S I I R R S L P A T L P Q C Q - 720

721 AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACAATCTGCAGATGCC
 -----+-----+-----+-----+-----+-----+-----+
 TCCGTCGCTTGTCTGGACGGGTGTTAATGTACACCTTATTAGTGTAGACGTCACGG
 A A N K T C P T N Y M W N N H I C R C L - 780

781 TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
 -----+-----+-----+-----+-----+-----+-----+
 ACCGAGTCCTTCTAAAATACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
 A Q E D F M F S S D A G D D S T D G F H - 840

841 ATGACATCTGTGGACCAACAAGAGCTGGATGAAGAGACCTGTGTCAGTGTCTGCAGAG
 -----+-----+-----+-----+-----+-----+-----+
 TACTGTAGACACCTGGTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGCTCTC
 D I C G P N K E L D E E T C Q C V C R A - 900

901 CGGGGCTTCGGCCCTGCCAGCTGTGGACCCCAAGAACTAGACAGAACTCATGCCAGT
 -----+-----+-----+-----+-----+-----+-----+
 GCCCGAAGCCGACGGTCGACACCTGGGGTGTTCCTTGATCTGTCTTTGAGTACGGTCA
 G L R P A S C G P H K E L D R N S C Q C - 960

961 GTGTCTGTAAAACAACAACTCTTCCCCAGCCAATGTGGGCCAACCGAGAATTGATGAAA
 -----+-----+-----+-----+-----+-----+-----+
 CACAGACATTTTGTGGAAGGGGTCGGTTACACCCCGGTTGGCTCTTAAACTACTTT
 MATCH WITH FIG. 1D 1020

FIG. 1C

MATCH WITH FIG. 1C

V C K N K L F P S Q C G A N R E F D E N -
 ACACATGCCAGTGTGTATGTAAGAACCCTGCCCCAGAAATCAACCCCTAAATCCTGGAA 1021
 TGTGTACGGTCACACATACATTTCTTGGACGGGTCTTTAGTTGGGAATTTAGGACCTT 1080
 T C Q C V C K R T C P R N Q P L N P G K -
 AATGTGCCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTTAAAGGAAGAGTTCC 1081
 TTACACGGACACTTACATGTCTTTCAGGTGTCTTTACGAACAATTTTCCTTTCTCAAGG 1140
 C A C E C T E S P Q K C L L K G K K F H -
 ACCACCAACATGCAGCTGTACAGACGGCCATGTACGAACCGCCAGAGGCTTGTGAGC 1141
 TGGTGGTTTGTACGTCGACAAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG 1200
 H Q T C S C Y R R P C T N R Q K A C E P -
 CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCTTCATATTGGCAAGACCAC 1201
 GTCCTAAAGTATATCACTTCTTCACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG 1260
 G F S Y S E E V C R C V P S Y W Q R P Q -
 AAATGAGCCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTCTATTATGGAAACTGTGT

MATCH WITH FIG. 1E

FIG. 1D

MATCH WITH FIG. 1D

```

1261 -----+-----+-----+-----+-----+-----+-----+
TTTACTCGATTCTAACATGACACAAAAGGTCAAGTAGCTAAAGATAATACCTTTTGACACA
      M   S   *
1321 -----+-----+-----+-----+-----+-----+-----+
TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCCTTGTGGGTCCATGCTAACAAAGACA
1380 -----+-----+-----+-----+-----+-----+-----+
ACGGTGTCACTCTTGACAGACACTGTCTCTCTGGAACACCCAGGTACGATTGTTTCTGT
AAAGTCTGTCTTTCCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG
1381 -----+-----+-----+-----+-----+-----+-----+
TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC
CAAAGGCCCTCTTGTAAGACTGGTTTTCTGCCAATGACCAACAGCCAAGATTTTCCTC
1441 -----+-----+-----+-----+-----+-----+-----+
GTTTTCCGGAGAACATTTCTGACCACAAAGACGGTTACTGGTTTGTGCGGTTCTAAAAGGAG
TTGTGATTTCTTTAAAGAAATGACTATATAATTTATTTCCACTAAAAATATTGTTTCTGC
1501 -----+-----+-----+-----+-----+-----+-----+
AACACTAAAGAAATTTTCTTACTGATATATTAAATAAAGGTGATTTTATATAACAAAGACG
ATTCAATTTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAATATTTTATATCAT
1561 -----+-----+-----+-----+-----+-----+-----+
TAAGTAAAAAATATCGTTGTTGTTAACCATTTTGAGTGACACTAGTTATAAAAATATAGTA
GCAAAAATATGTTTAAAAATAAAATGAAAATTTGTATTTATAAAAAAATAAAAAAAA
1621 -----+-----+-----+-----+-----+-----+-----+
CGTTTATACAAAATTTATTTTACTTTTAAACATAAAATATTTTTTTTTT
1674 -----+-----+-----+-----+-----+-----+-----+

```

FIG. 1E

```

1  CGAGGCCACGGCTTATGCAAGCAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT
   -----+-----+-----+-----+-----+-----+-----+
71  AGATGAACATCATGACTGTACTCTACCCAGAATATTGGAATAATGTACAAGTGTCAAGTAAG
   -----+-----+-----+-----+-----+-----+-----+
      M T V L Y P E Y W K M Y K C Q L R
121 GAAAGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGACAGAAGAGAC
   -----+-----+-----+-----+-----+-----+-----+
      K G G W Q H N R E Q A N L N S R T E E T
181 TATAAAATTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG
   -----+-----+-----+-----+-----+-----+-----+
      I K F A A A H Y N T E I L K S I D N E W
241 GAGAAAGACTCAATGCATGCCACGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGT
   -----+-----+-----+-----+-----+-----+-----+
      R K T Q C M P R E V C I D V G K E F G V
301 CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTGCTG
   -----+-----+-----+-----+-----+-----+-----+
      A T N T F F K P P C V S V Y R C G G C C

```

FIG. 2A

361 CAATAGTGGGCTGCAGTGCATGAACACCAGCAGGCTACCTCAGCAAGACGTTATT
 N S E G L Q C M N T S T S Y L S K T L F

421 TGAATACAGTGCCTCTCTCAAGGCCCAACCAAGTAACAATCAGTTTGGCCAATCA
 E I T V P L S Q G P K P V T I S F A N H

481 CACTTCCTGCCGATGCTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAG
 T S C R C M S K L D V Y R Q V H S I I R

541 ACGTTCCCTGCCAGCAACACTACCACAGTGTCAAGCAGCGAACAAGACCTGCCCCACCAA
 R S L P A T L P Q C Q A A N K T C P T N

601 TTACATGTGGAATAATCACATCTGCAGATGCCCTGGCTCAGGAAGATTTATGTTTCCTC
 Y M W N N H I C R C L A Q E D F M F S S

661 GGATGCTGGAGTGACTCAACAGATGGATTCCATGACATCTGTGGACCAACAAGGAGCT
 D A G D D S T D G F H D I C G P N K E L

FIG. 2B

```

721  GGATGAAGAGACCTGTCAGTGTCTGTCAGAGCGGGCTTCGGCCTGCCAGCTGTGGACC
    -----+-----+-----+-----+-----+-----+-----+
    D E E T C C Q C V C R A G L R P A S C G P

781  CCACAAAGAACTAGACAGAACTCATGCCAGTGTGTCTGTAAACAACTCTTCCCCAG
    -----+-----+-----+-----+-----+-----+-----+
    H K E L D R N S C Q C V C K N K L F P S

841  CCAATGTGGGCCAACCGAGAAATTGATGAAACACATGCCAGTGTGTATGTAAAGAAG
    -----+-----+-----+-----+-----+-----+-----+
    Q C G A N R E F D E N T C Q C V C K R T

901  CTGCCCCAGAAATCAACCCCTAAATCCTGGAAATGTGCCCTGTGAATGTACAGAAAGTCC
    -----+-----+-----+-----+-----+-----+-----+
    C P R N Q P L N P G K C A C E C T E S P

961  ACAGAAATGCTTGTAAAGGAAAGAAAGTTCCACCACCAACATGCAGCTGTACAGACG
    -----+-----+-----+-----+-----+-----+-----+
    Q K C L L K G K K F H H Q T C S C Y R R

1021 GCCATGTACGAACCGCCAGAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG
    -----+-----+-----+-----+-----+-----+-----+
    P C T N R Q K A C E P G F S Y S E E V C

```

FIG. 2C


```

1081 TCGTTGTGCCCTTCATATTGGCAAGACCACAAATGAGCTAAGATTGTACTGTTTCCCA
      R C V P S Y W Q R P Q M S
1141 GTTCATCGATTTTCTATTATGGAACACTGTGTGCCACAGTAGAACTGTCTGTGAACAGA
1201 GAGACCCTTGTGGTCCCATGCTAACAAAGACAAAAGTCTGTCTTTCCCTGAACCATGTGGA
1261 TAACTTTACAGAAATGGACTGGAGCTCATCTGCAAAAGGCCTCTTGTAAGACTGGTTTT
1321 CTGCCAATGACCCAAACAGCCCAAGATTTTCCTCTTGTGATTTCTTTAAAGAATGACTATA
1381 TAATTTATTCCCACTAAATAATGTTTCTGCAATTCATTTTATAGCAACAACAATTGGT
1441 AAAACTCACTGTGATCAATATTTTATATCATGCAAAATATGTTTAAATAAATGAAAA
1501 TTGTATTATAAAAAAATAAAAAA

```

FIG. 2D

```

1                               50
Pdga .MRTLACLLL LGGYLAHL AEEAIPREV IERLARSQIH SIRDQLRLE
Pdgb MNRCAWA.LFL SLCCYLRVLS AEGDPIPEEL YEMLSHSIR SFDDLQRLH
Vegf .....MNFL SWVHWSLALL LY..... .LHAKWSQA
Vegf2 .....MTV LYPEYWKMYK CQ..... .LRKGGWQH

51                               100
Pdga IDSVGSEDSL DTSRAHGVH ATKHVPEKRP LPIRRKRSI. ....EEAVP
Pdgb GDP.GEEDGA ELDNMTRSH SCGELES... .LARGRRSLG SLTIAEPAMI
Vegf APMAE..... .GGGQ NHHEVVKFMD .VYQR.....
Vegf2 REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK.....

101                              150
Pdga AVCKTRTVIY EIPRSQVDPT SANFLIWPCC VEVKRCTGCC NTSSVKQGPS
Pdgb AECKTRTEVF EISRLIDRT NANFLVMPCC VEVQRCGGCC NNRNVQCRPT
Vegf SYCHPIETLV DIFQEYPDEI ..EYIFKPSC VPLMRCCGCC NDEGLECVPT
Vegf2 TQCMPPREVC I DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT

151                              200
Pdga RVHHRVKVA KVEYVRKKPK LKEVQVRLEE HLEQAC.... AT.....
Pdgb QVQLRPVQVR KIEIVRKKPI FKCATVTLED HLACKG.... ETVAARPVT
Vegf EESNITMQIM RIK.PH..QG QHIGEMSFLQ HNKCECRPKK DRARQEKSV
Vegf2 STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCRCMSKL DVYRQVHSII

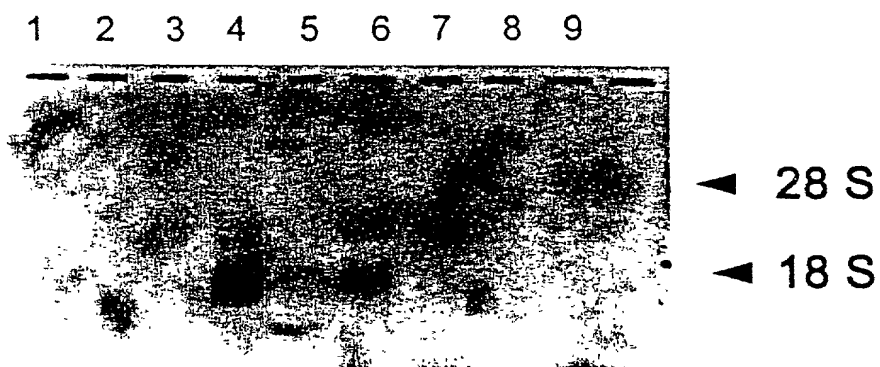
```

FIG. 3A

PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN EACH PAIR OF GENES IS SHOWN IN THE FOLLOWING TABLE				
	PDGF α	PDGF β	VEGF	VEGF2
PDGF α				
PDGF β	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

FIG.4

Expression of VEGF2 mRNA in Human Breast Tumor Cells



Lane 1. normal breast tissue
Lane 2. breast tumor tissue
Lane 3-9. breast tumor cell lines.

FIG.5

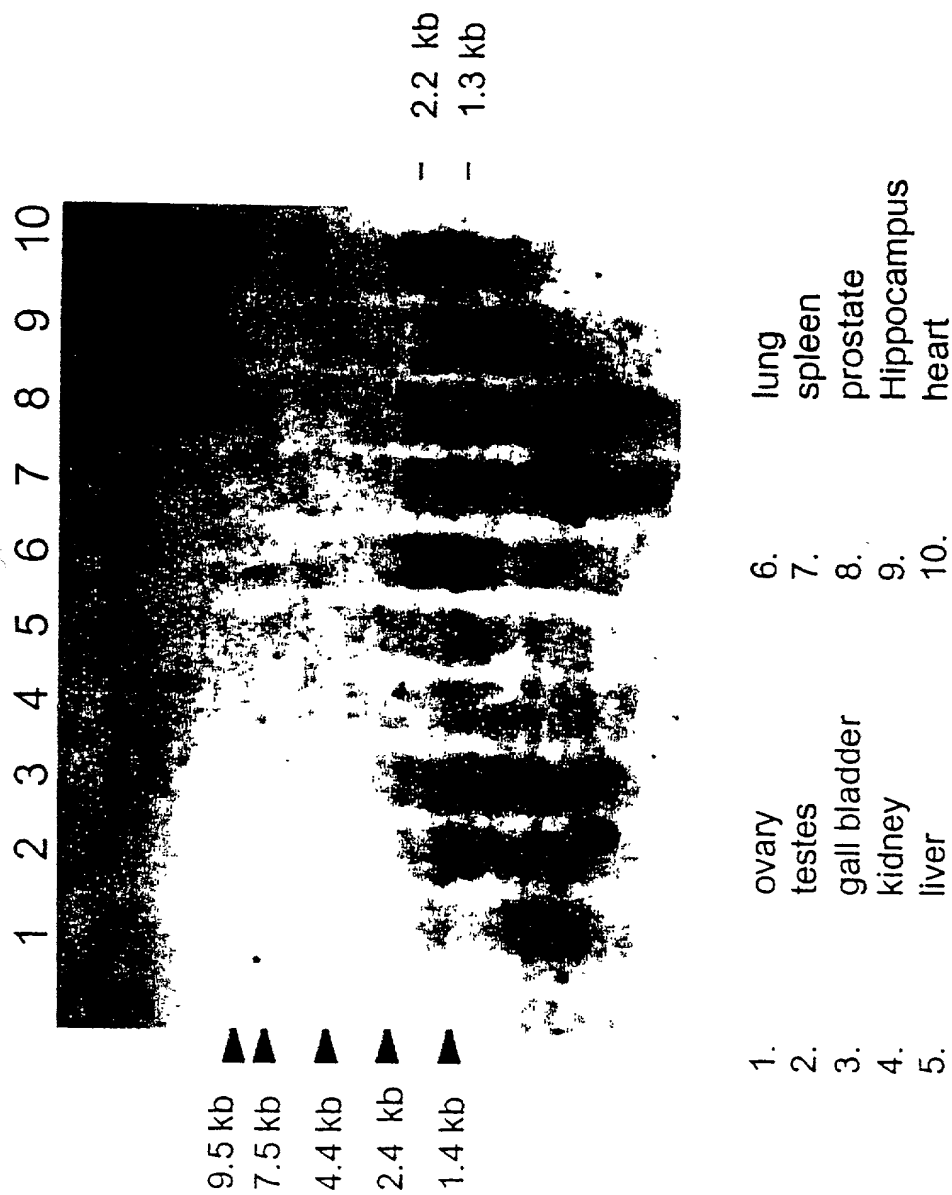
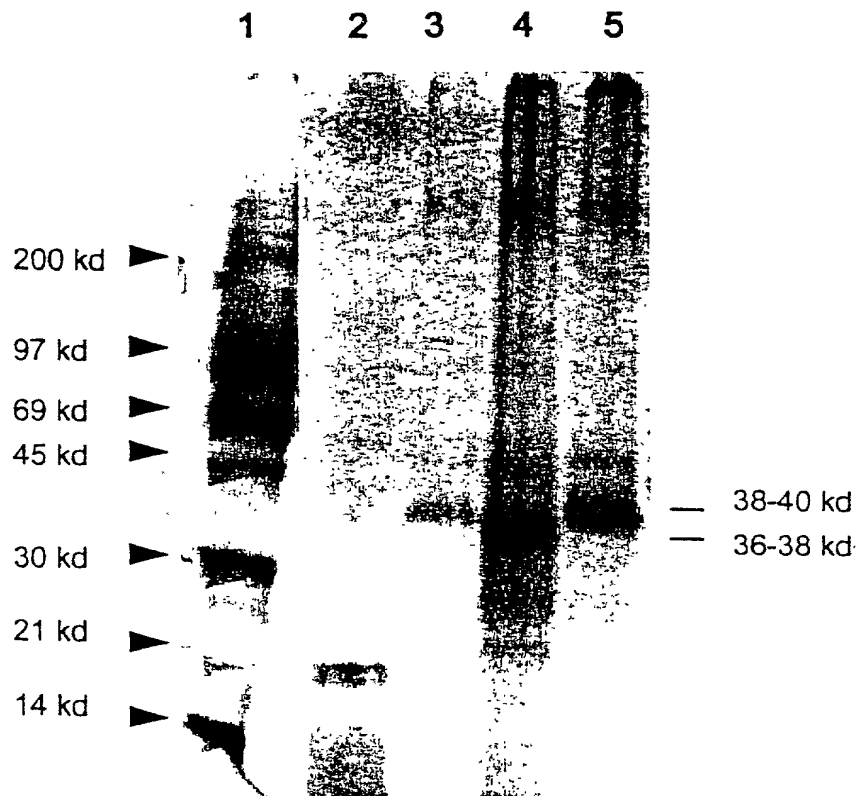


FIG.6

Expression of VEGF2 mRNA in human adult tissues.

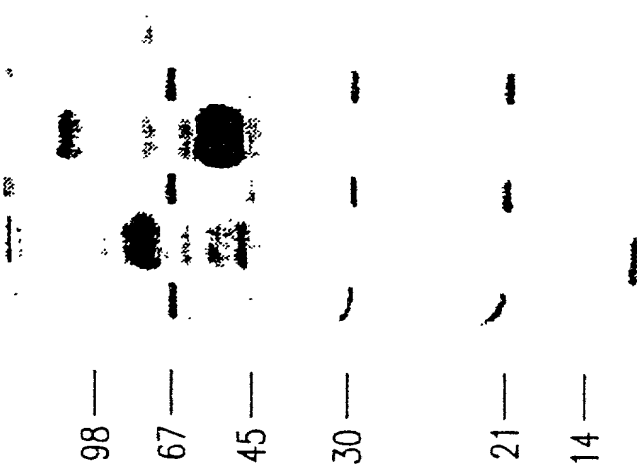


Lane 1: 14-C and rainbow M.W. marker
 Lane 2: FGF control
 Lane 3: VEGF2 (M13-reverse & forward primers)
 Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
 Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

FIG.7

non-reducing gel

M 1 M 2 M



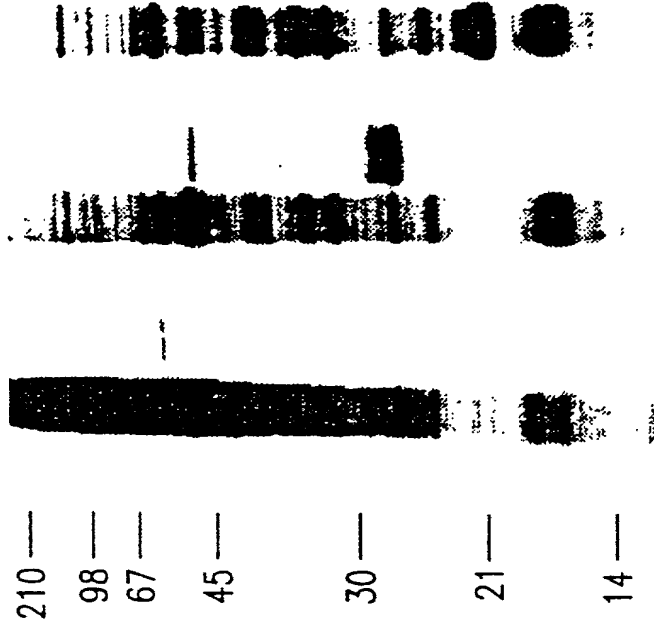
Lane M
Lane 1
Lane 2

Marker
vector medium
VEGF2 medium

FIG. 8A

reducing gel

M 1 2 M 3 4 M

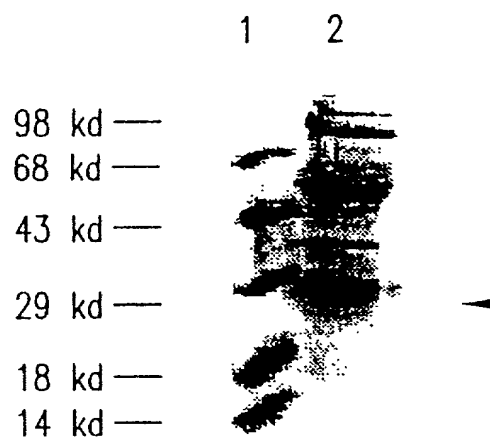


Lane M:
Lane 1:
Lane 2:
Lane 3:
Lane 4:

Marker
vector Cytoplasm
vector medium
VEGF2 Cytoplasm
VEGF2 medium

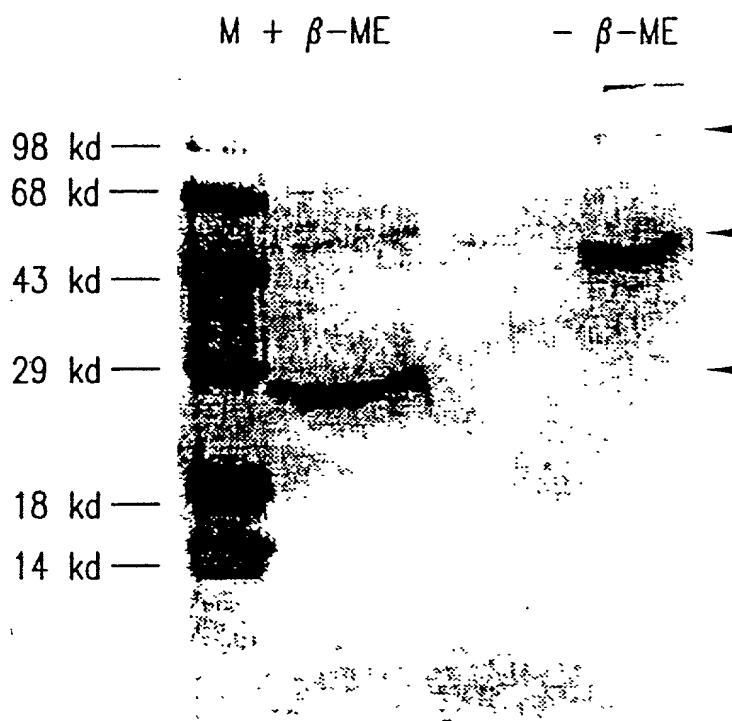
FIG. 8B

FIG.9



Lane 1: Molecular weight marker
Lane 2: Precipitates containing VEGF2.

FIG.10



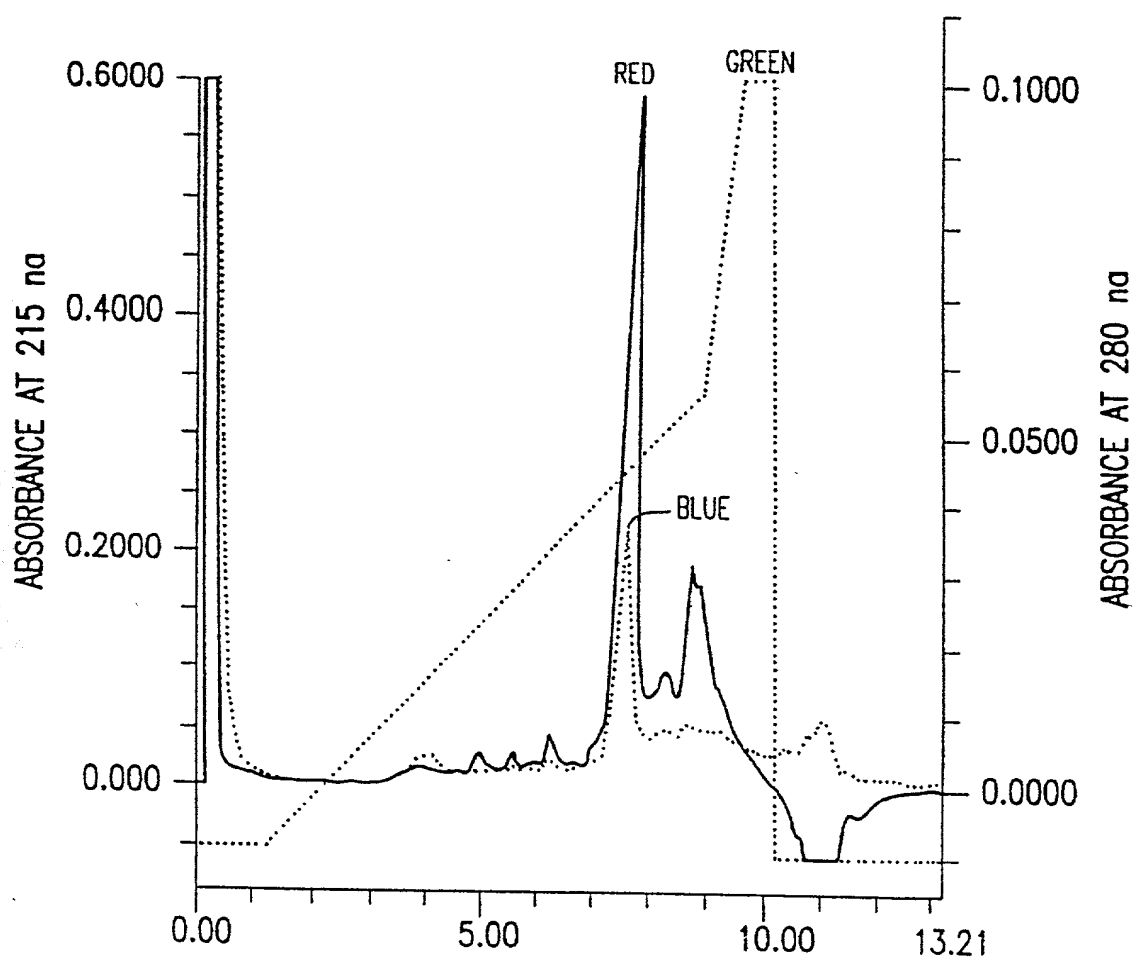


FIG. 11

FIG.12

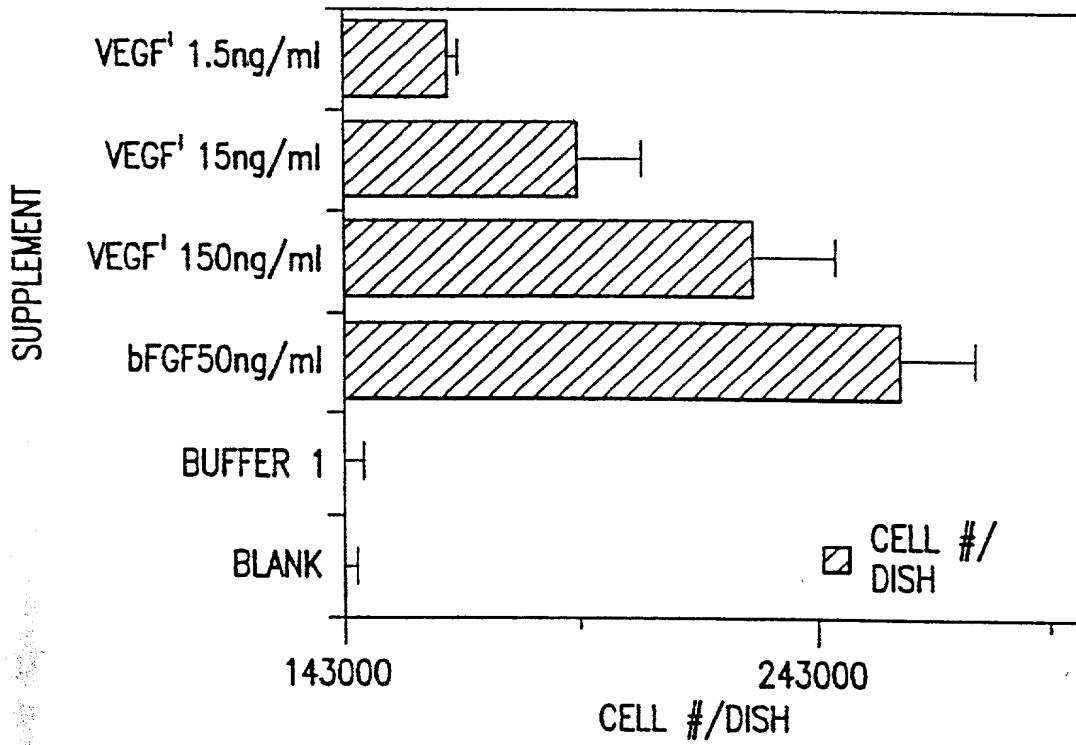


FIG.13

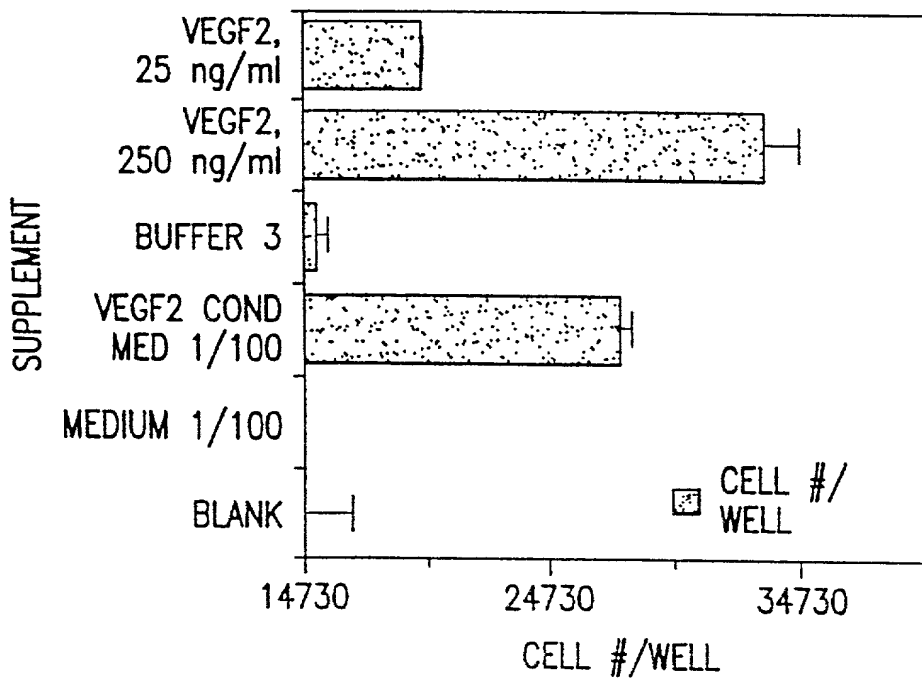


FIG.14A

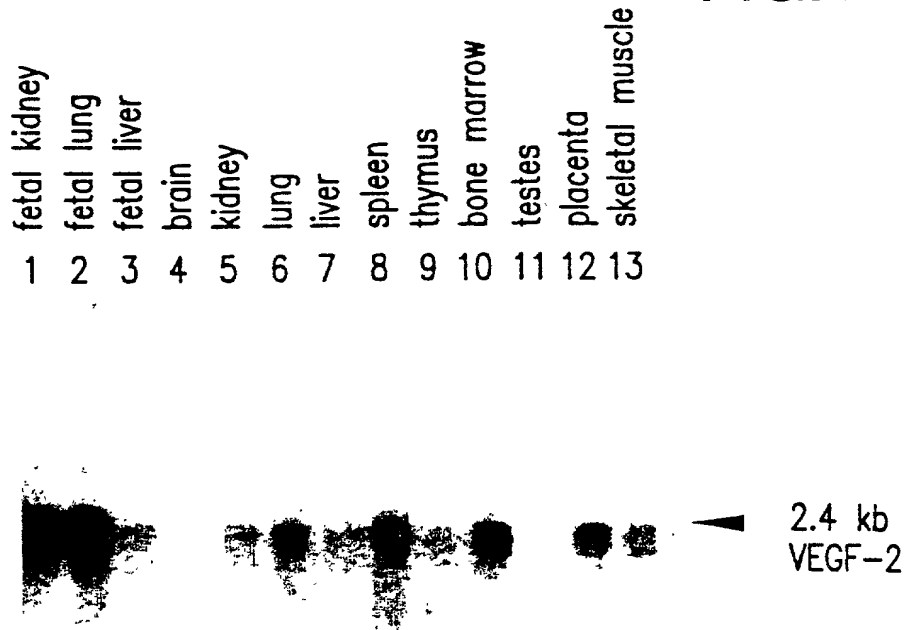
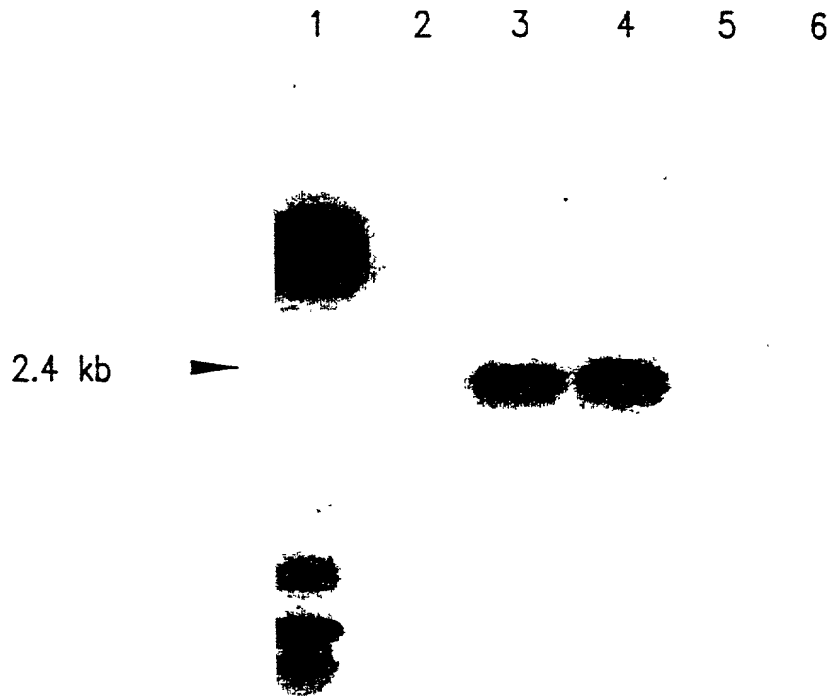


FIG.14B

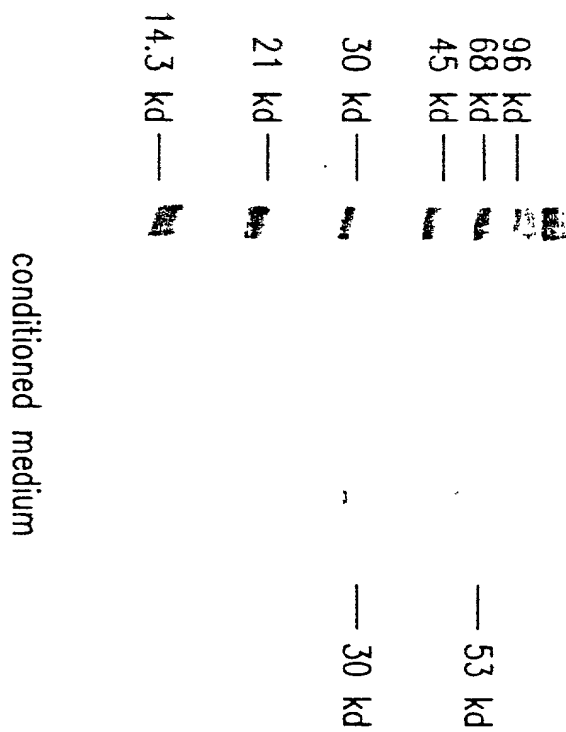




1. Molecular Weight Marker
2. umbelical vein endothelial cells
3. aortic smooth muscle cells
4. Dermal fibroblast

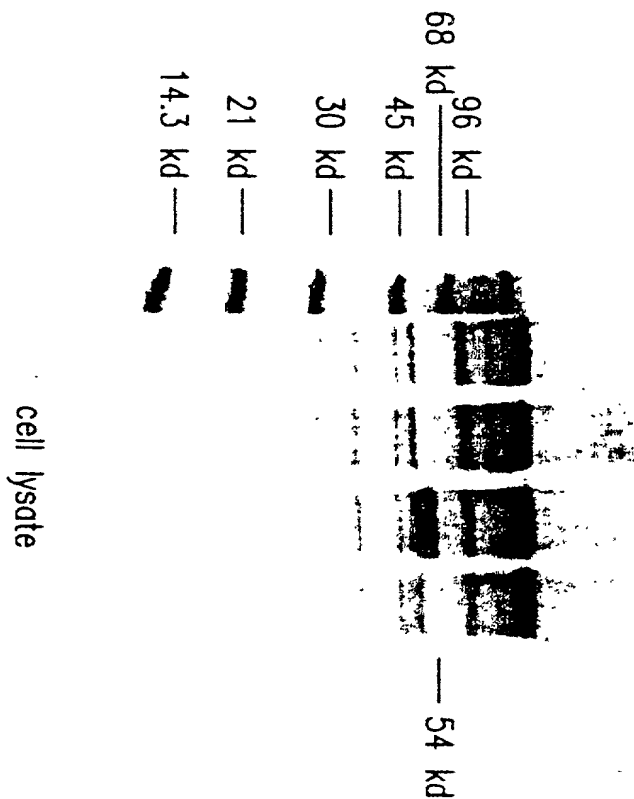
FIG.15

FIG.16A



1. m.w. marker
2. blank
3. control protein-HA
4. vector control
5. VEGF2-HA

FIG.16B



1. m.w. marker
2. blank
3. control protein-HA
4. VEGF2-HA
5. vector control

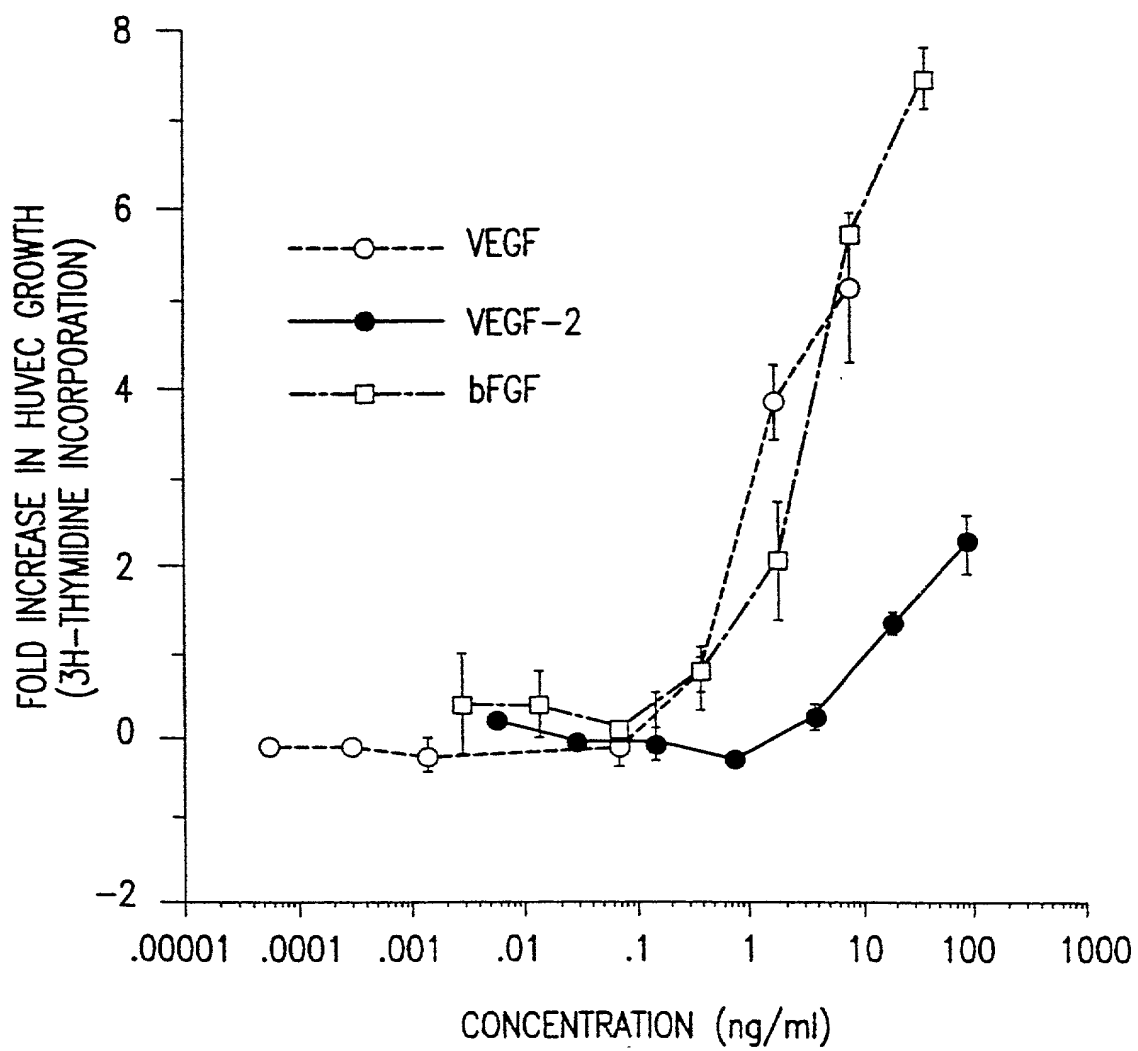


FIG.17

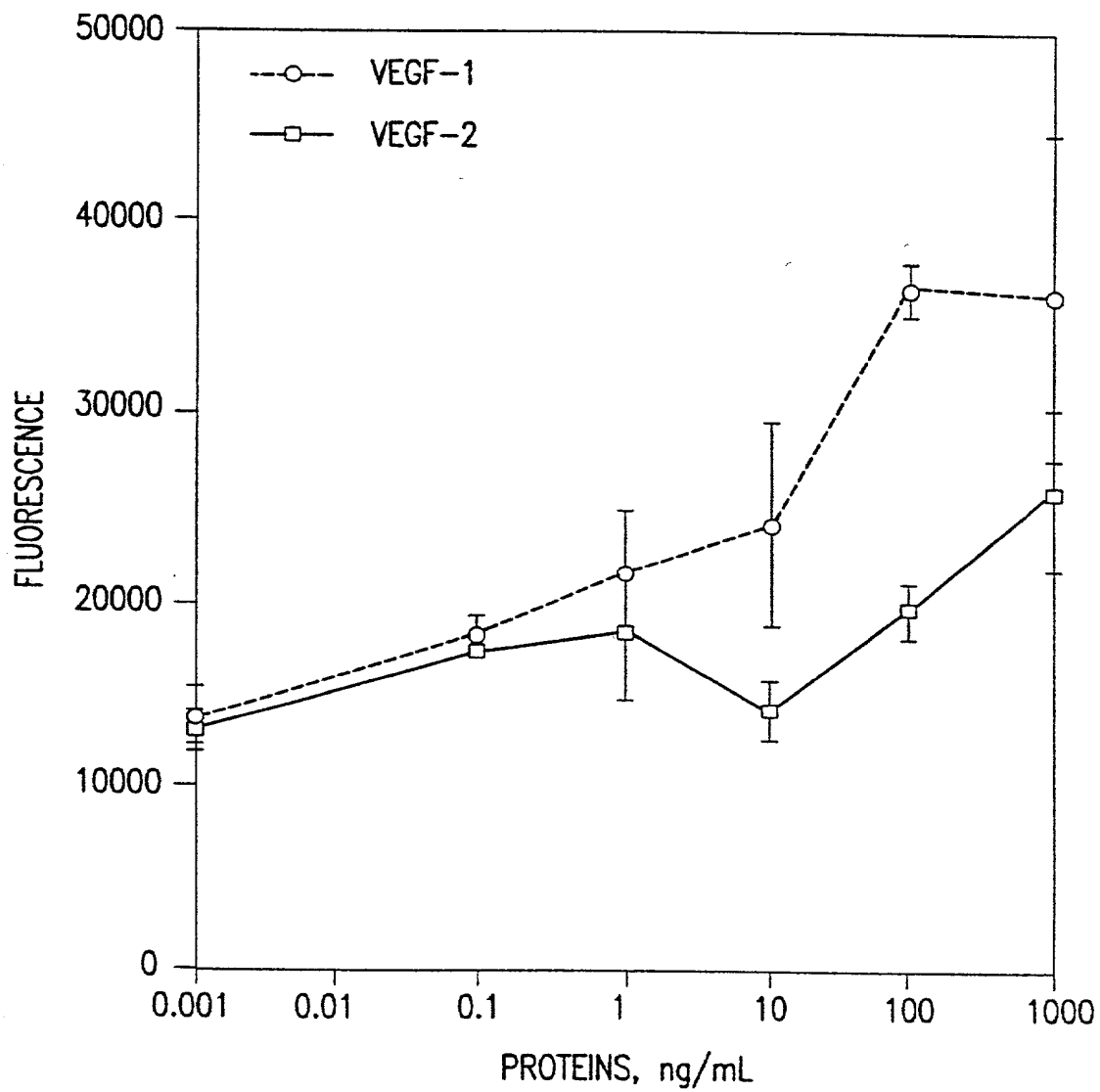


FIG.18

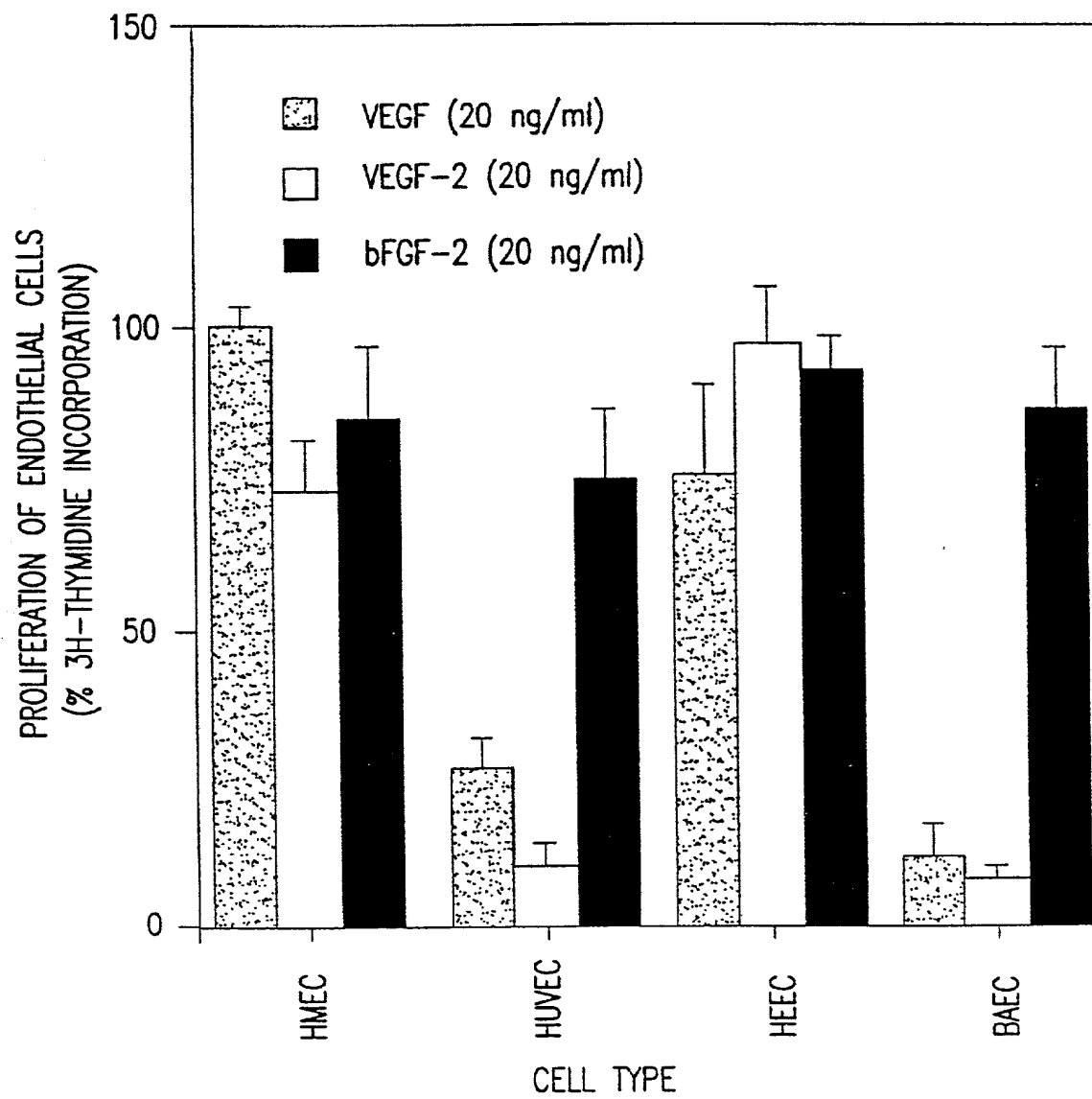


FIG.19

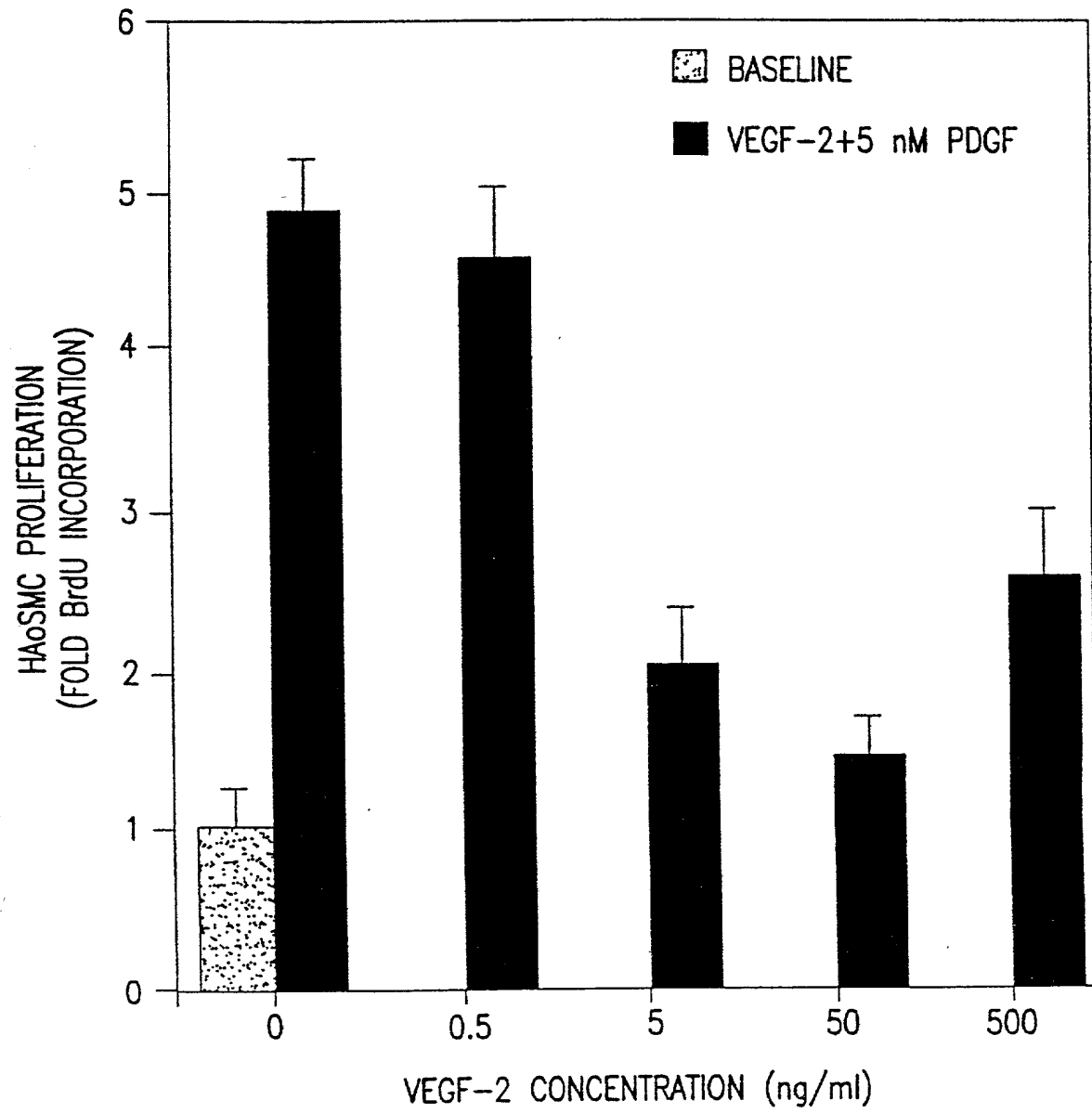


FIG.20A

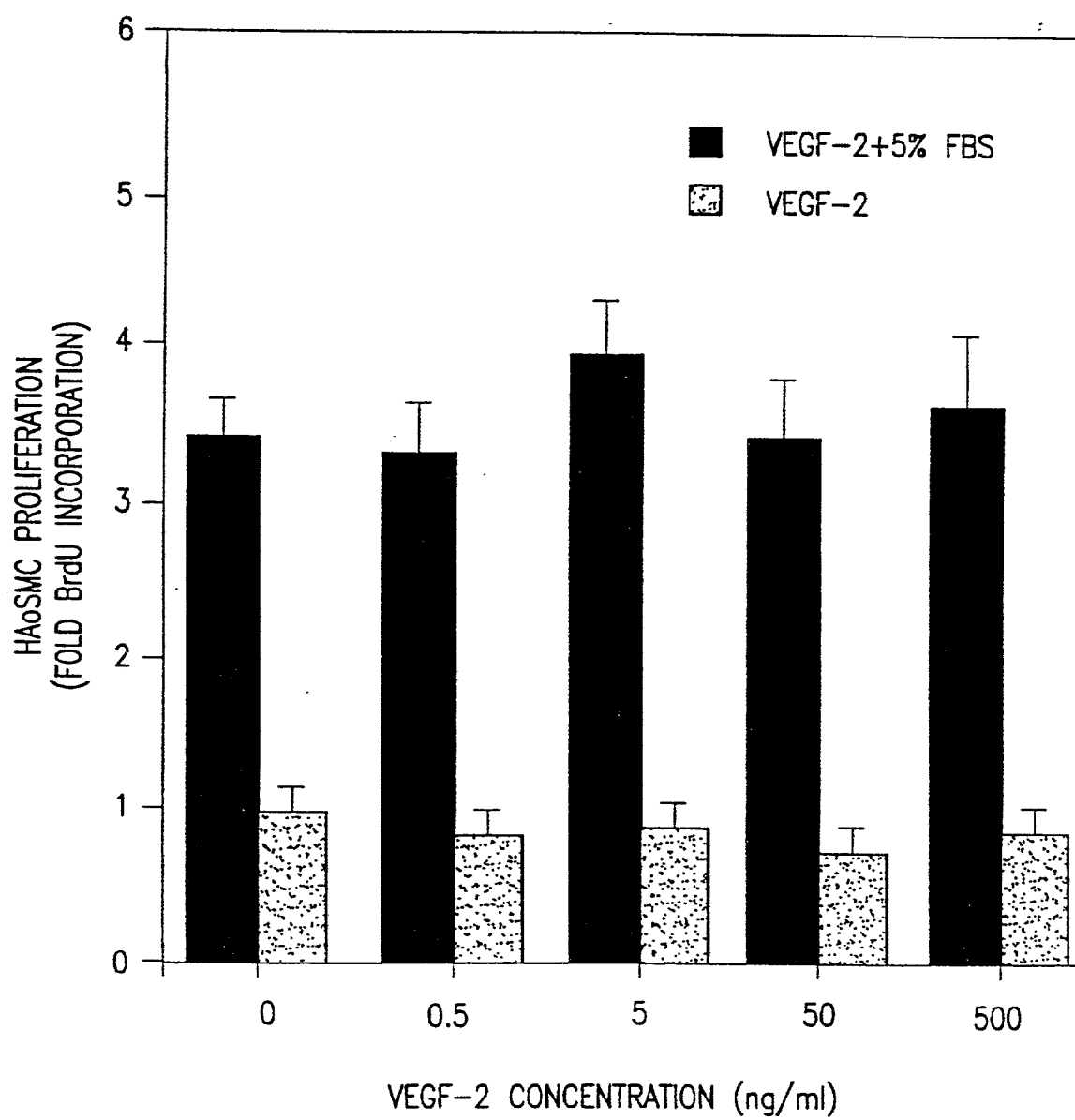


FIG.20B

FIG.21A

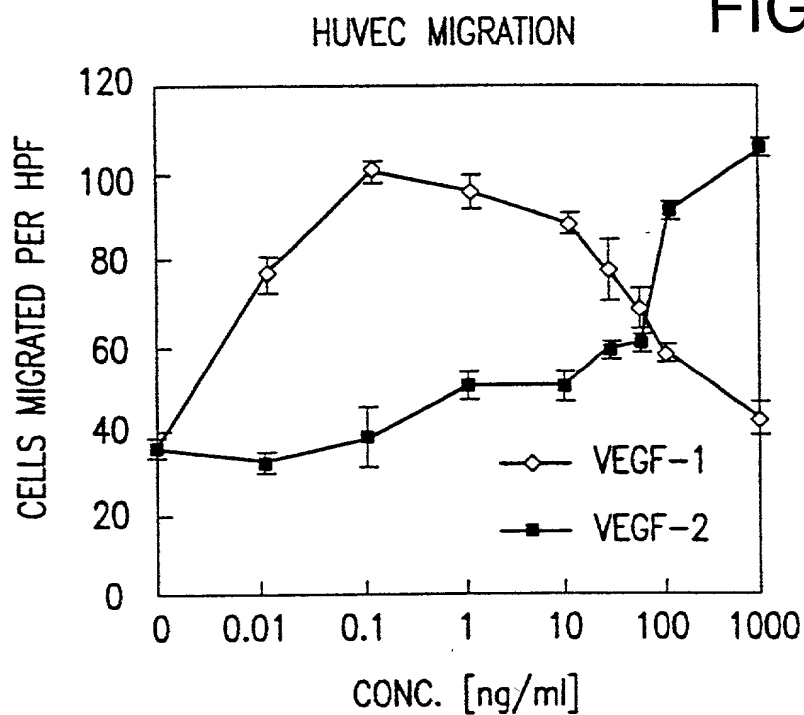
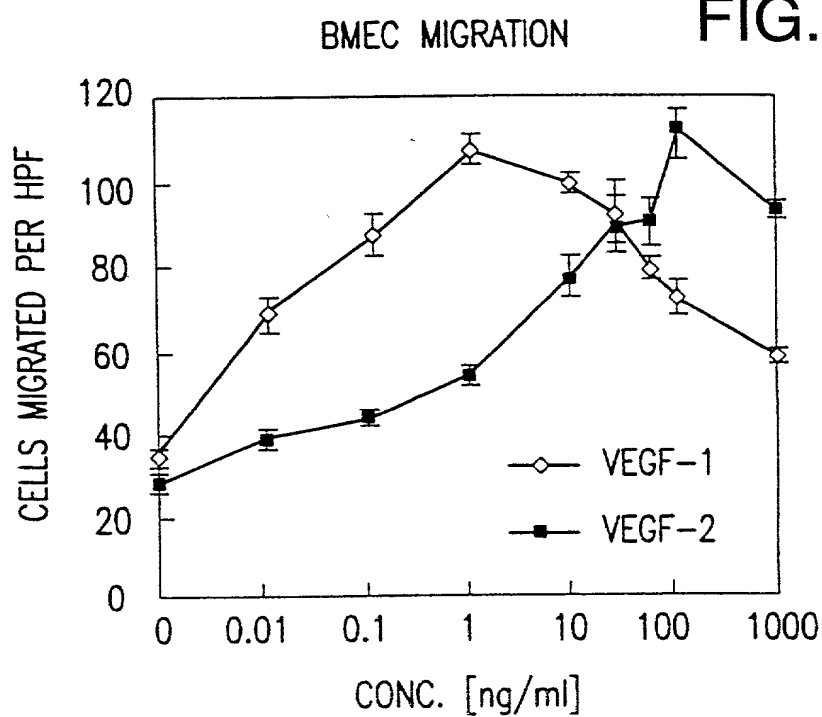


FIG.21B



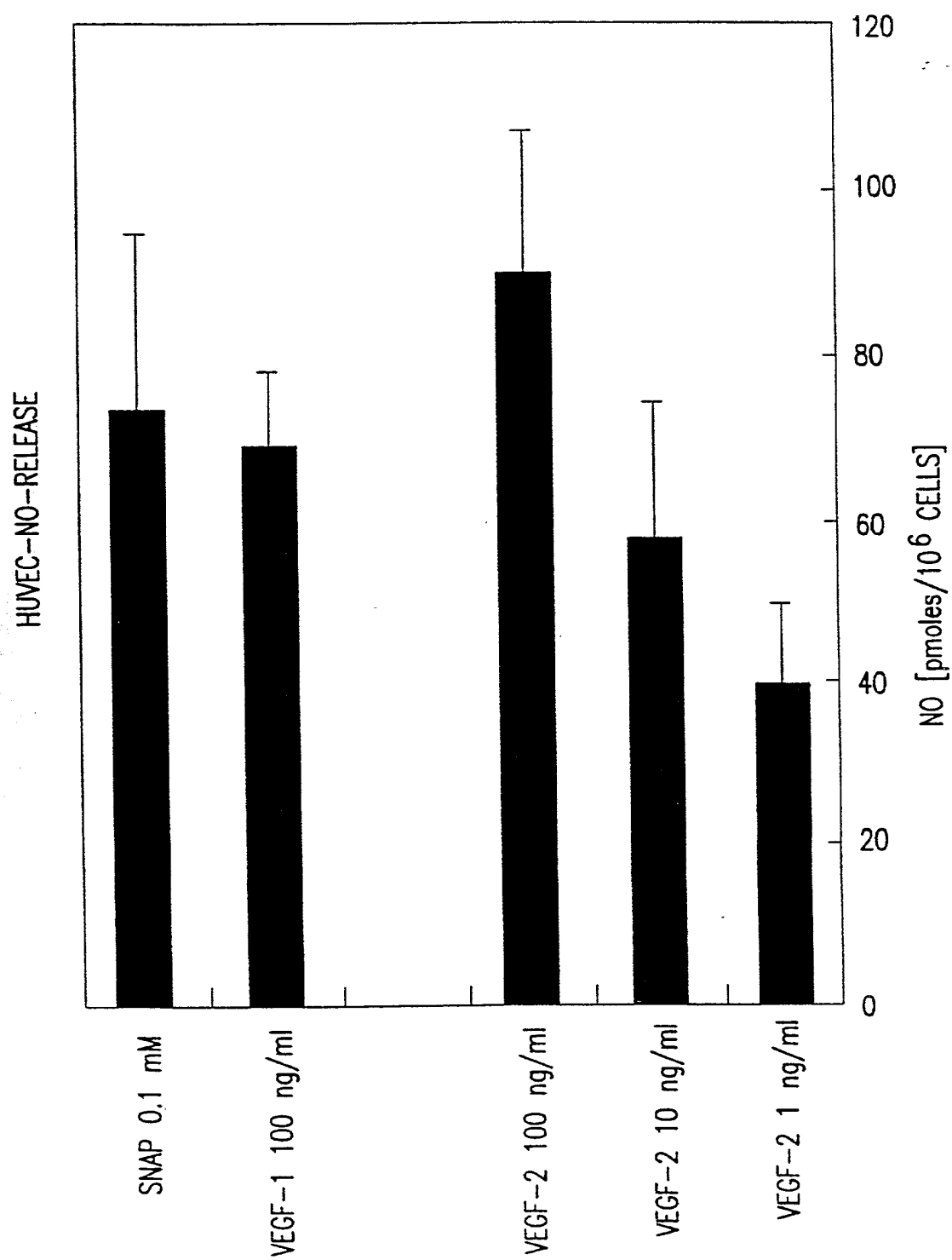


FIG.22

FIG.23

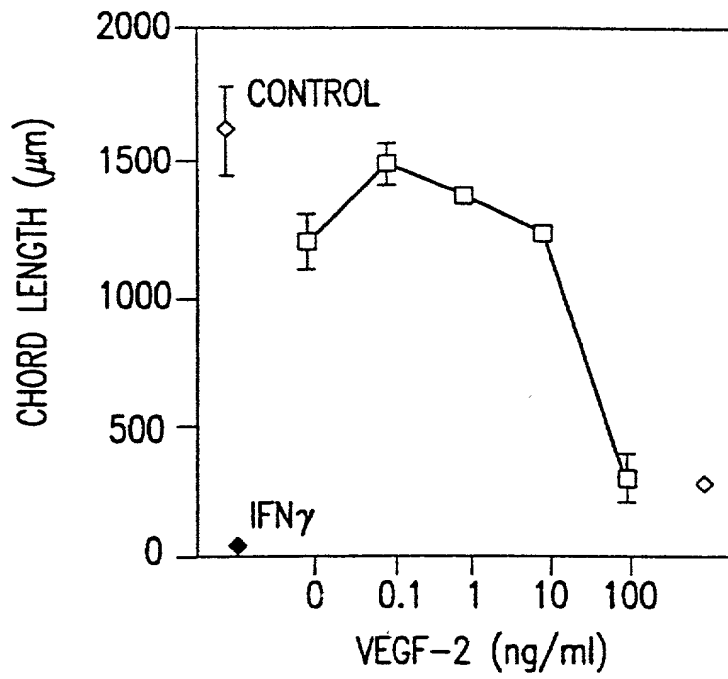


FIG.24

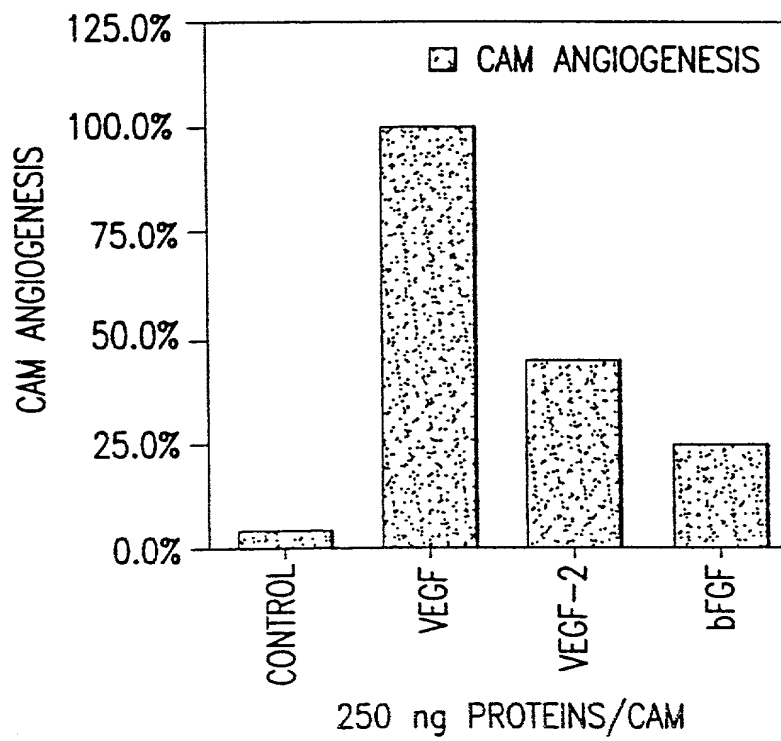


FIG.25A

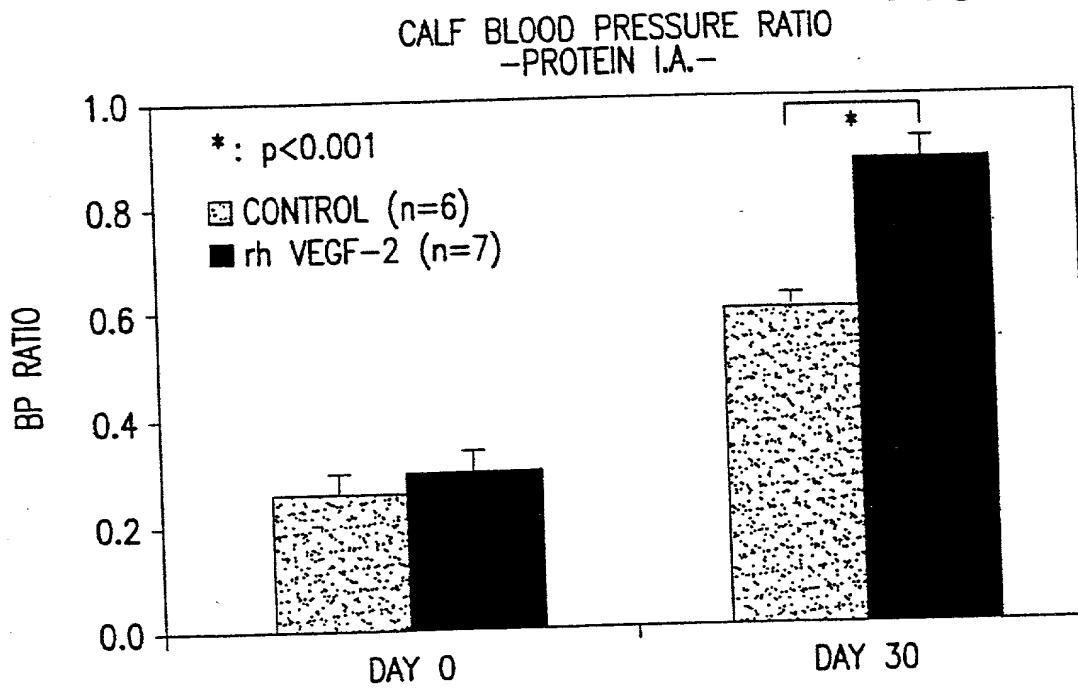
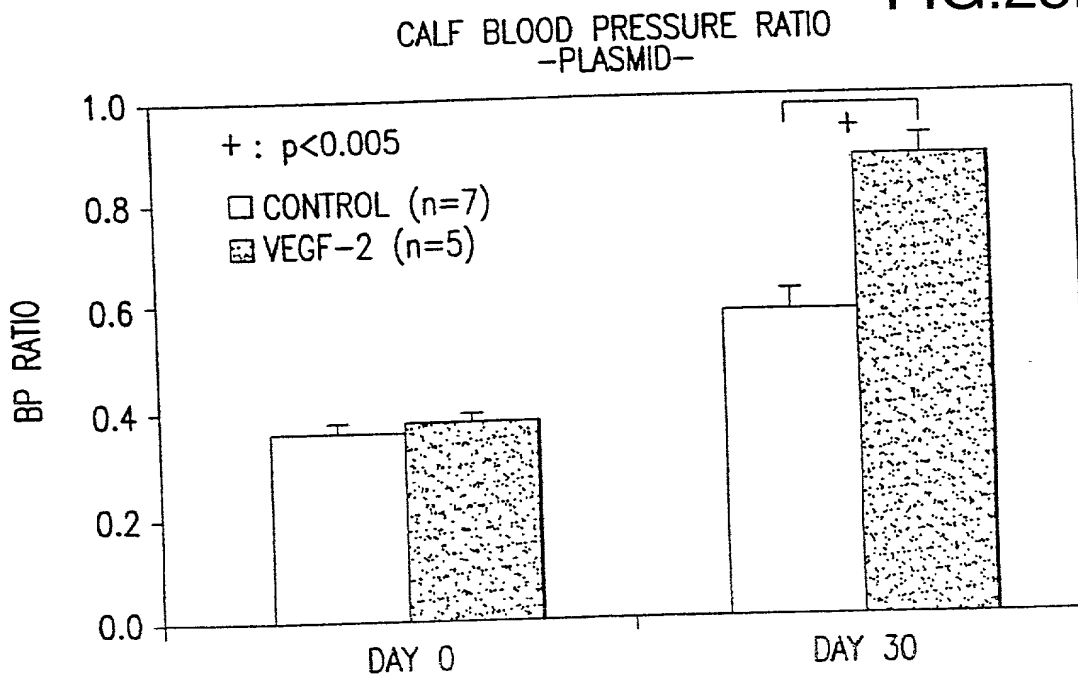


FIG.25B



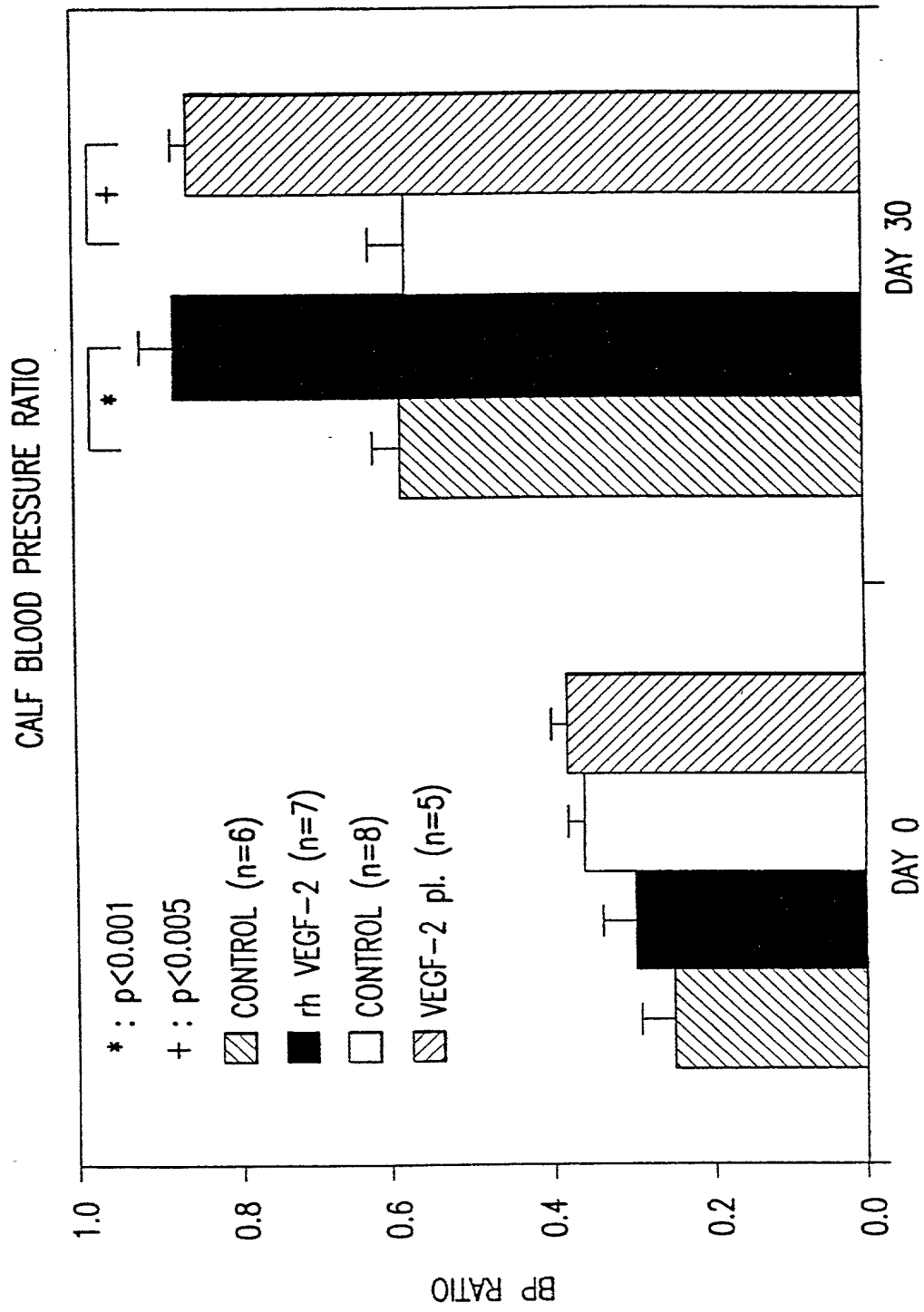
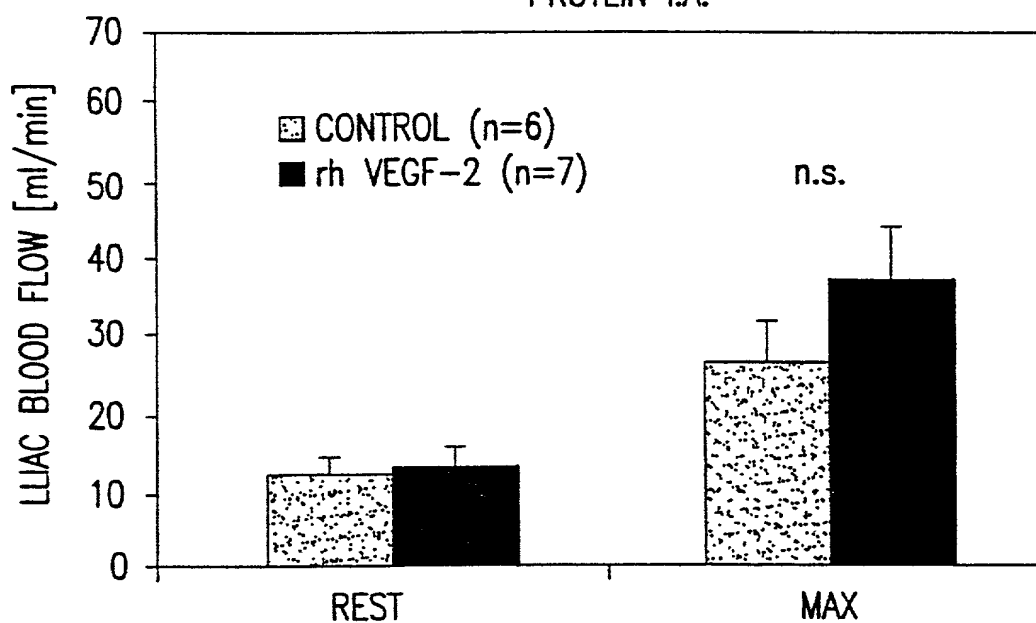


FIG.25C

33/47

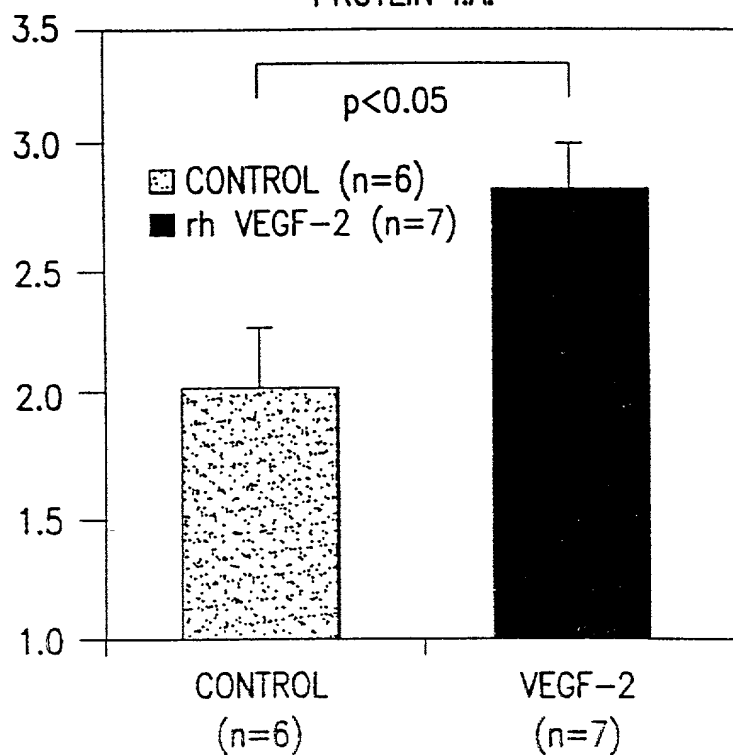
LLIAC BLOOD FLOW
-PROTEIN I.A.-

FIG.25D



LLIAC FLOW RESERVE
-PROTEIN I.A.-

FIG.25E



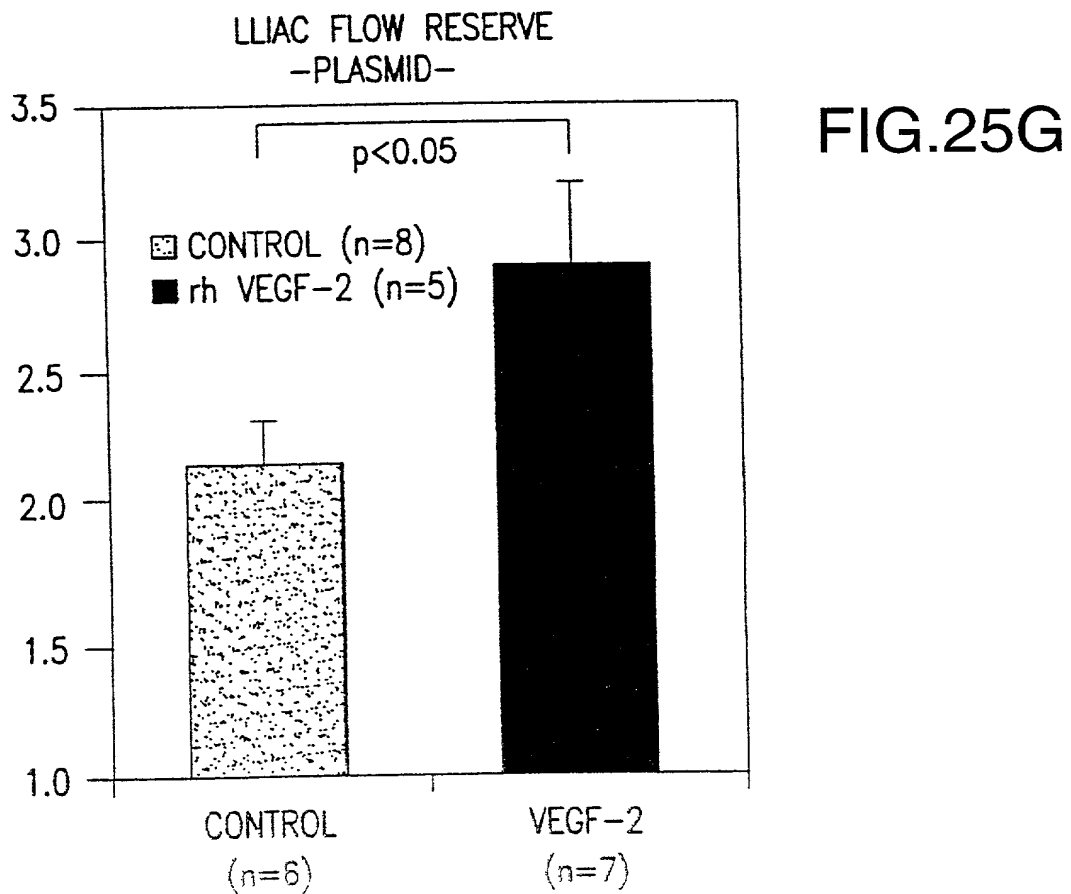
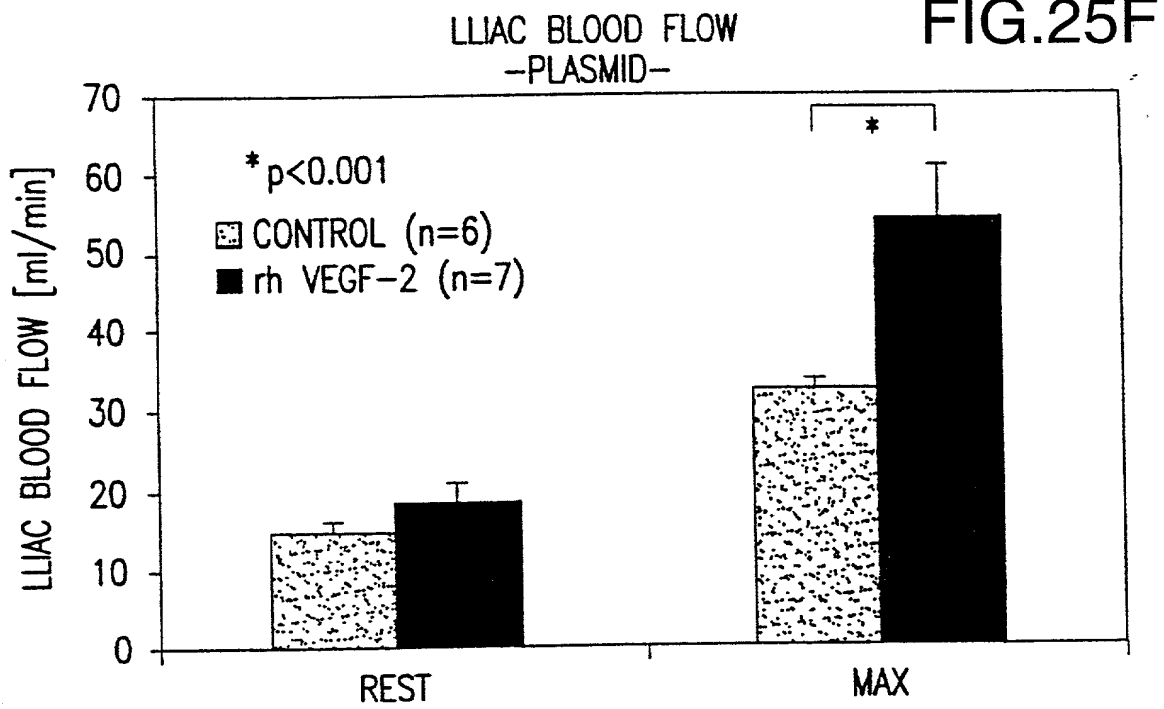


FIG.25H

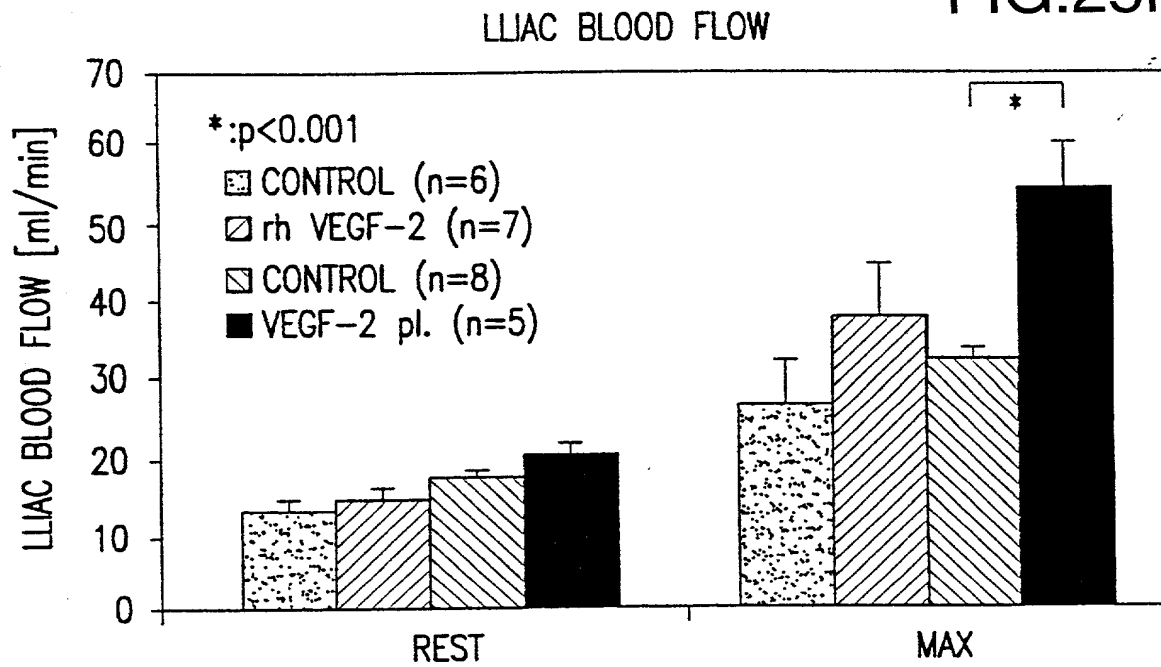
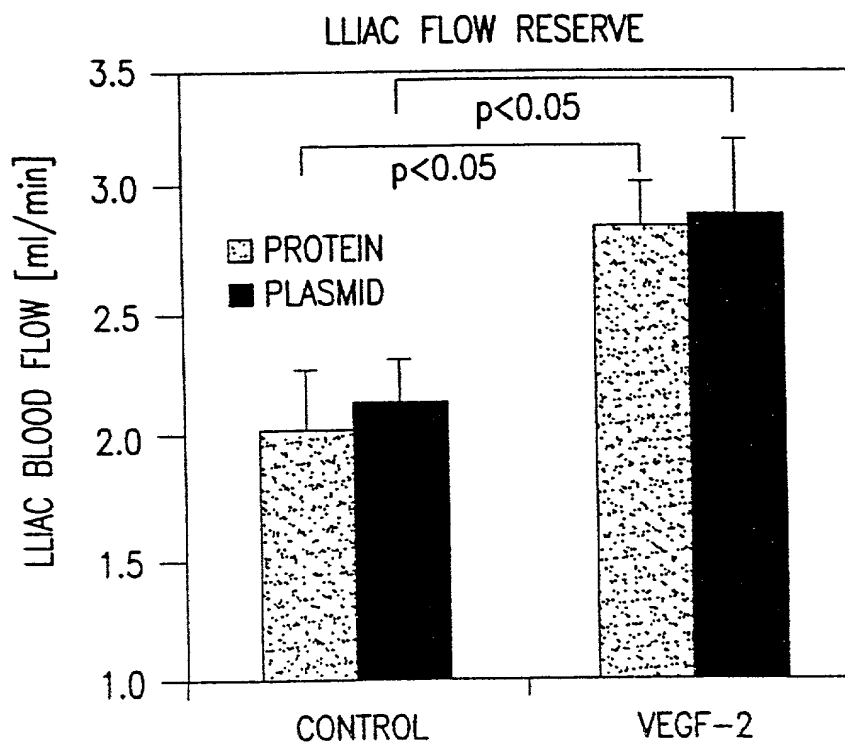


FIG.25I



ANGIOGRAPHIC SCORE
-PROTEIN I.A.-

FIG.25J

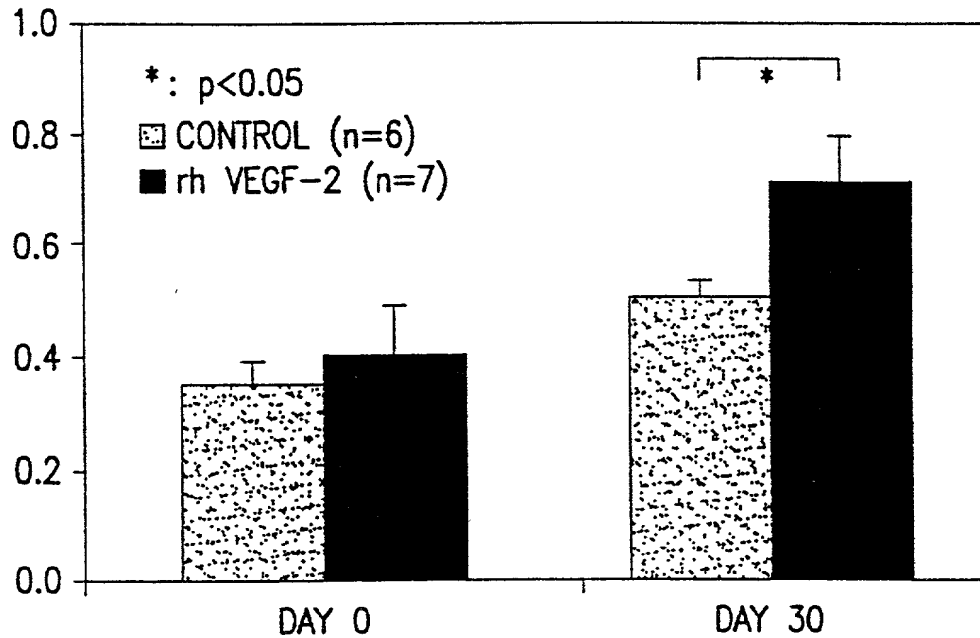
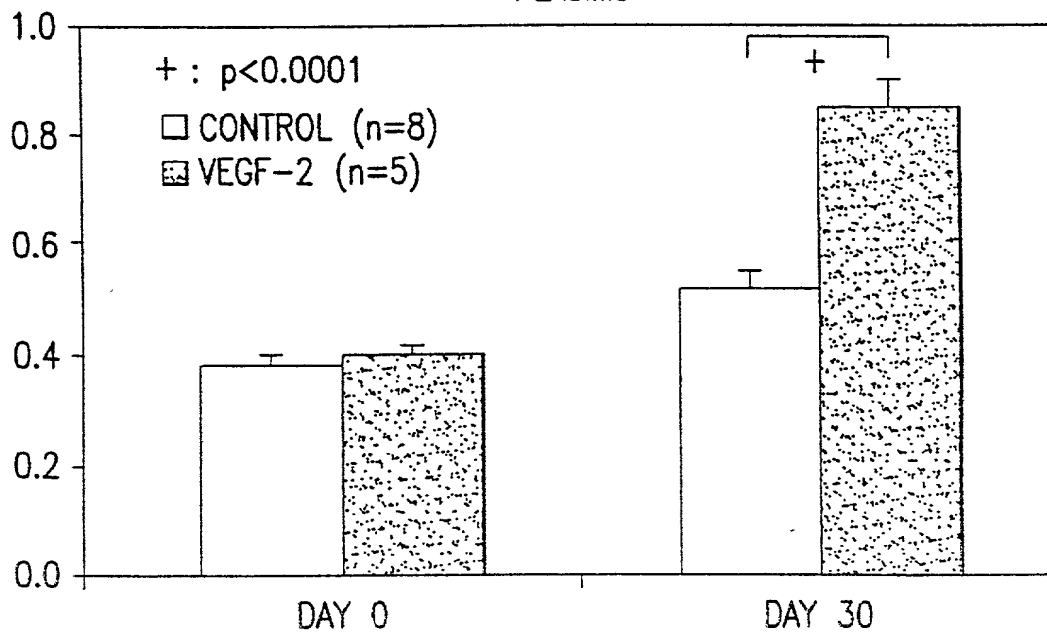
ANGIOGRAPHIC SCORE
-PLASMID-

FIG.25K



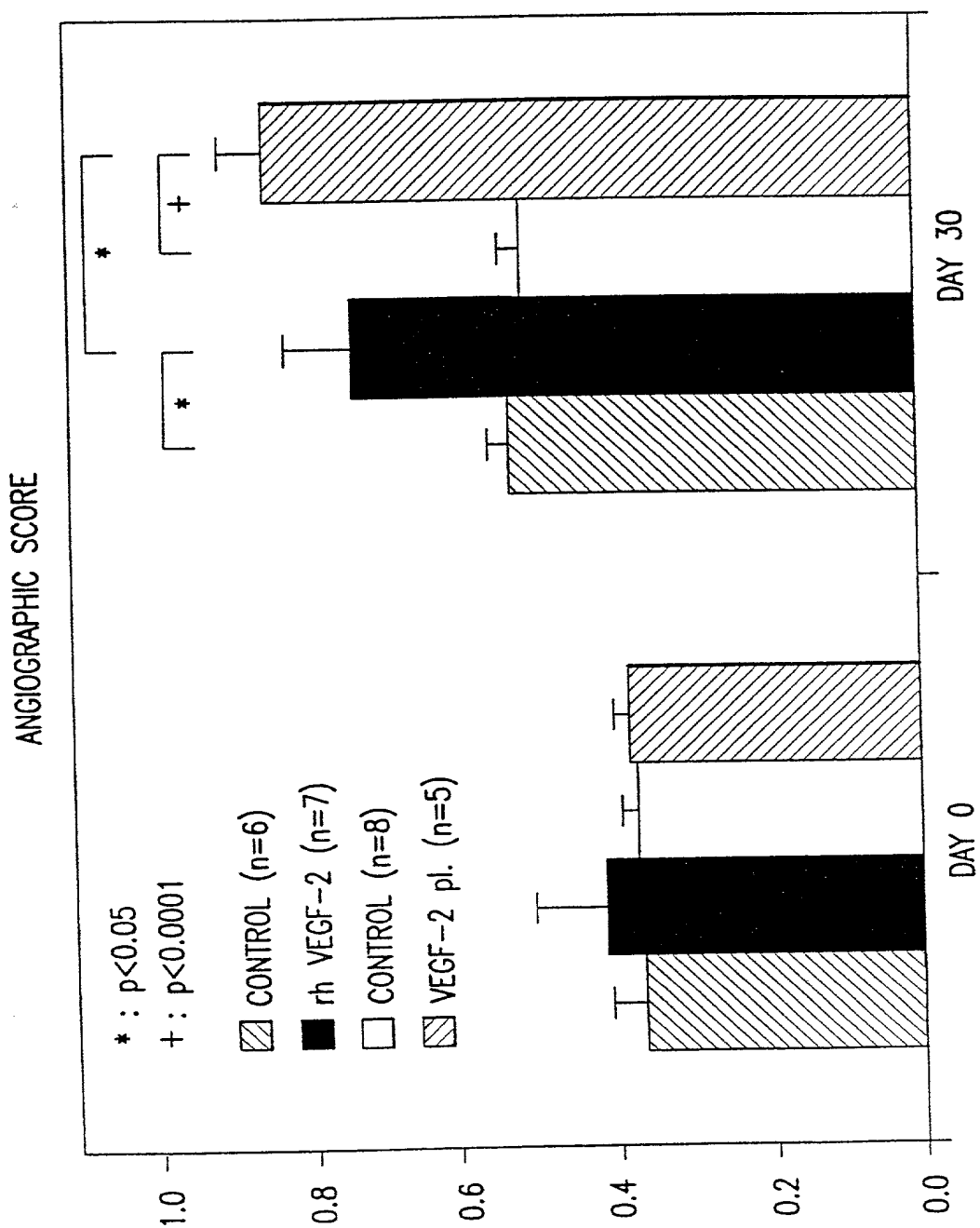


FIG.25L

FIG.25M

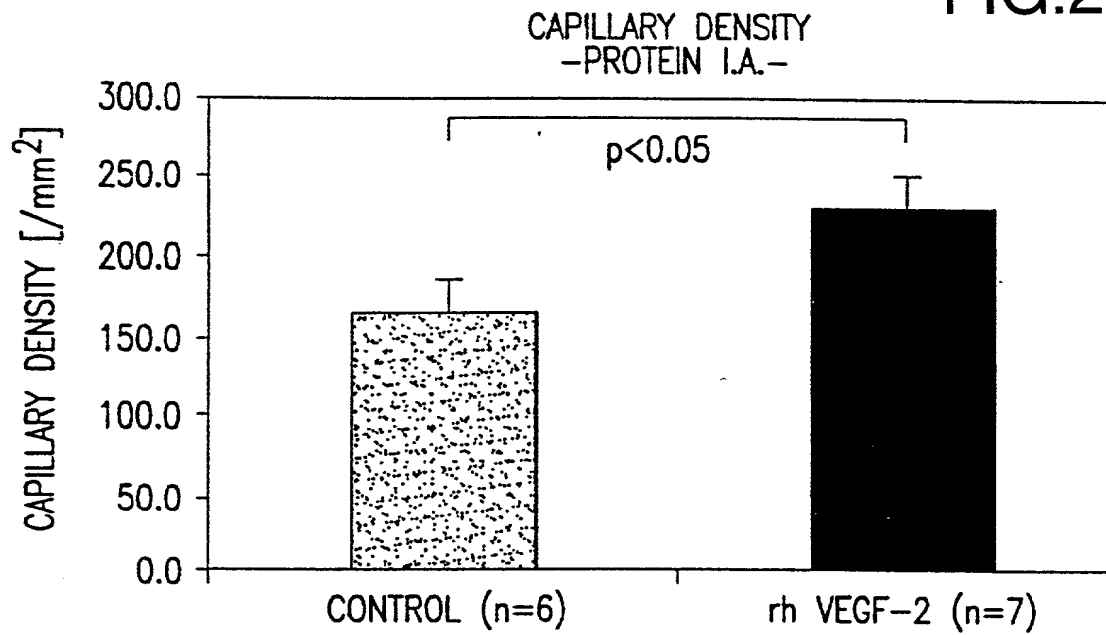
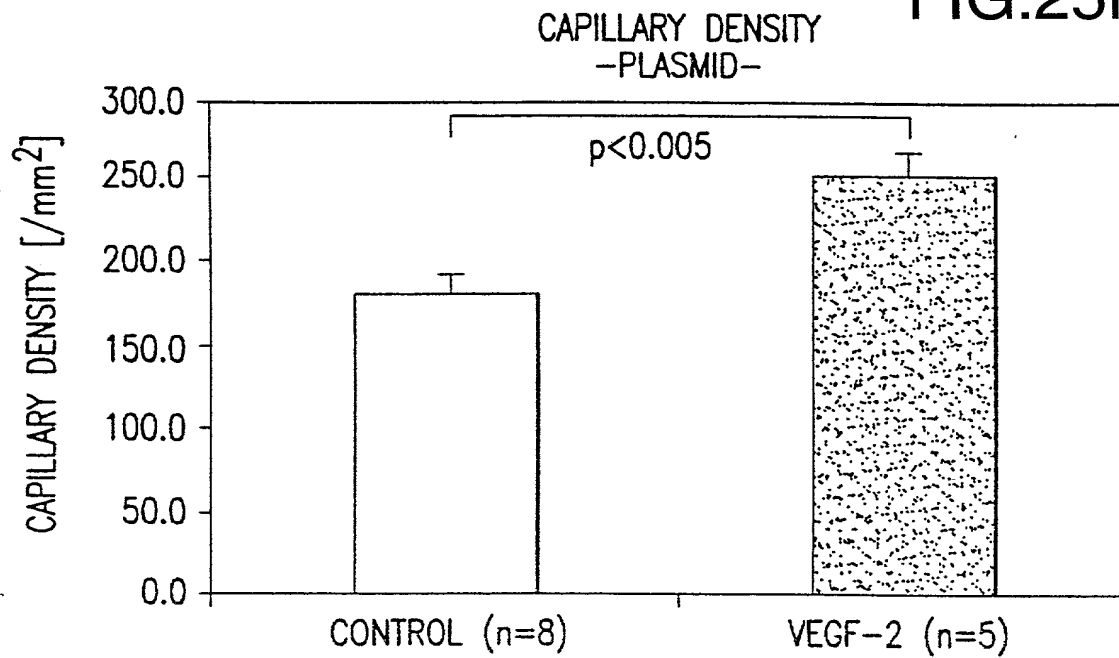
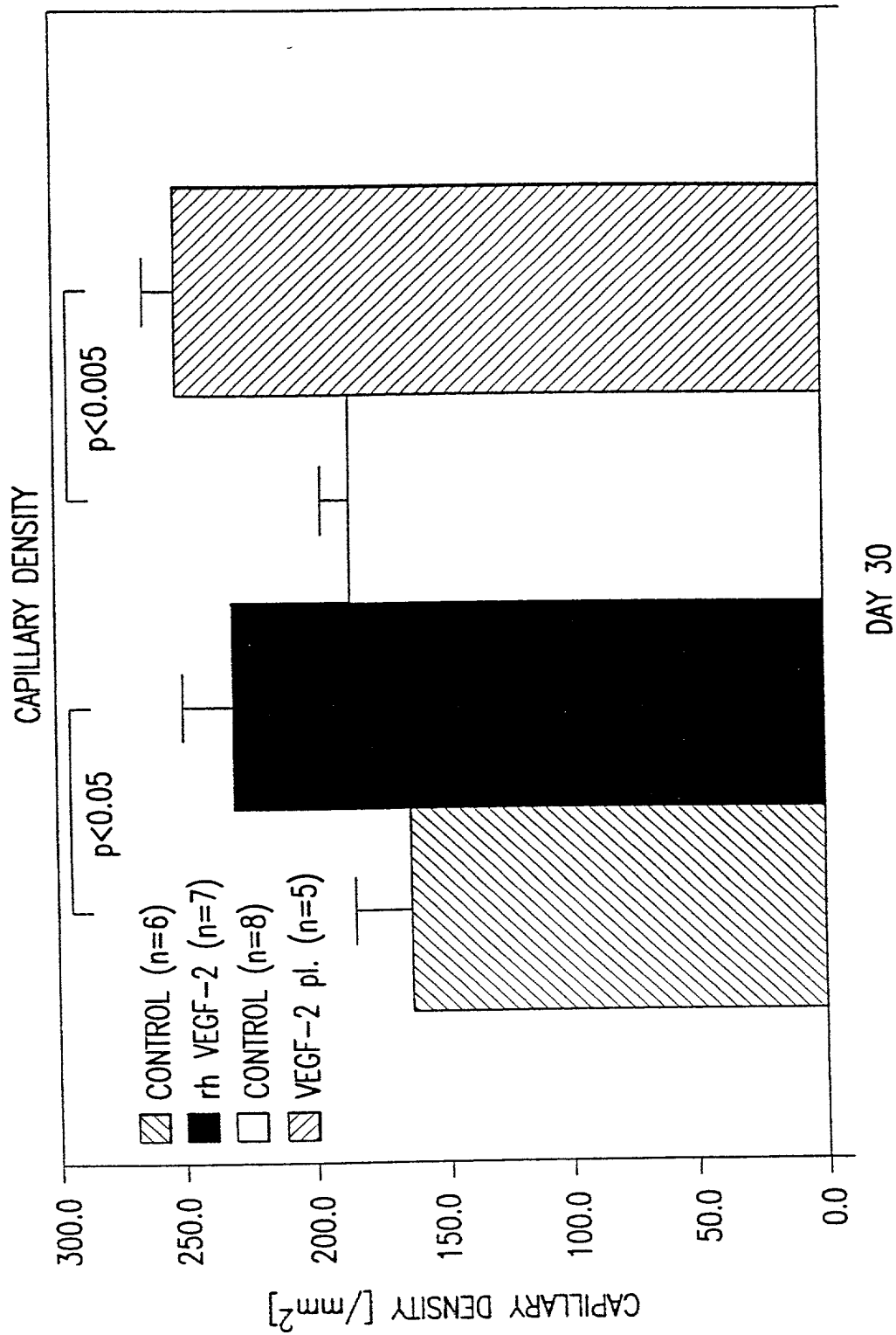


FIG.25N





40/47

FIG.26A

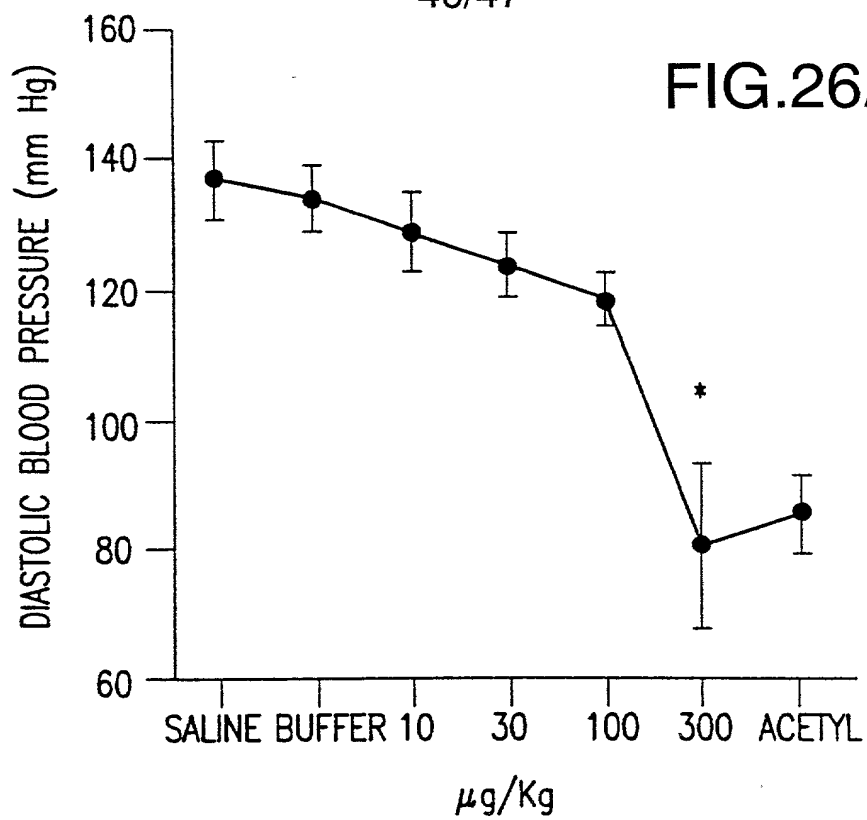
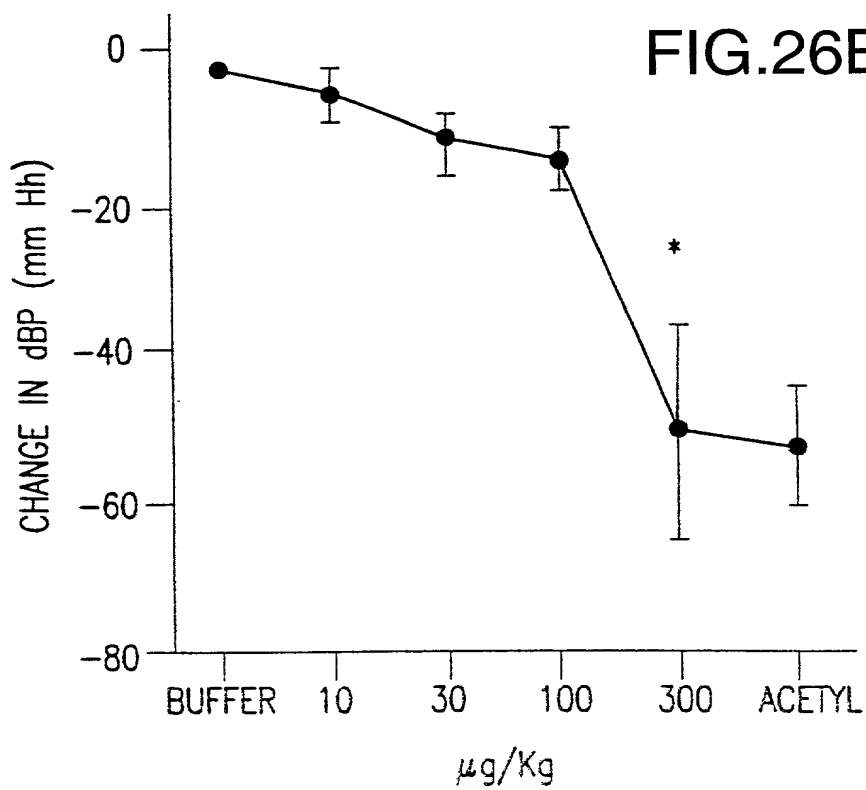


FIG.26B



41/47

FIG.26C

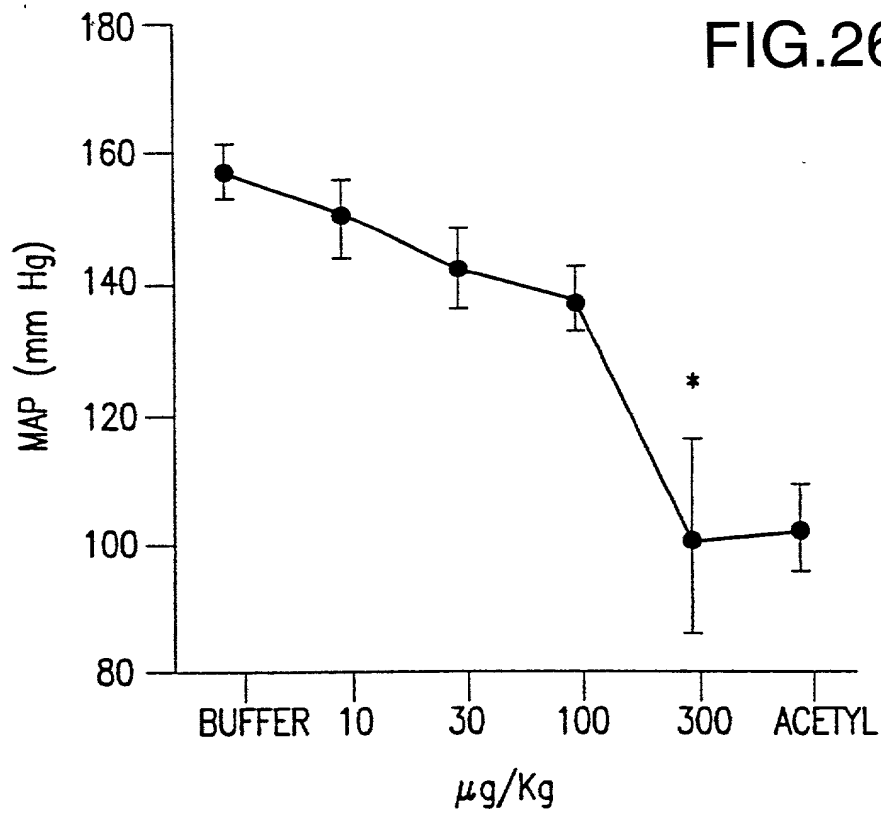
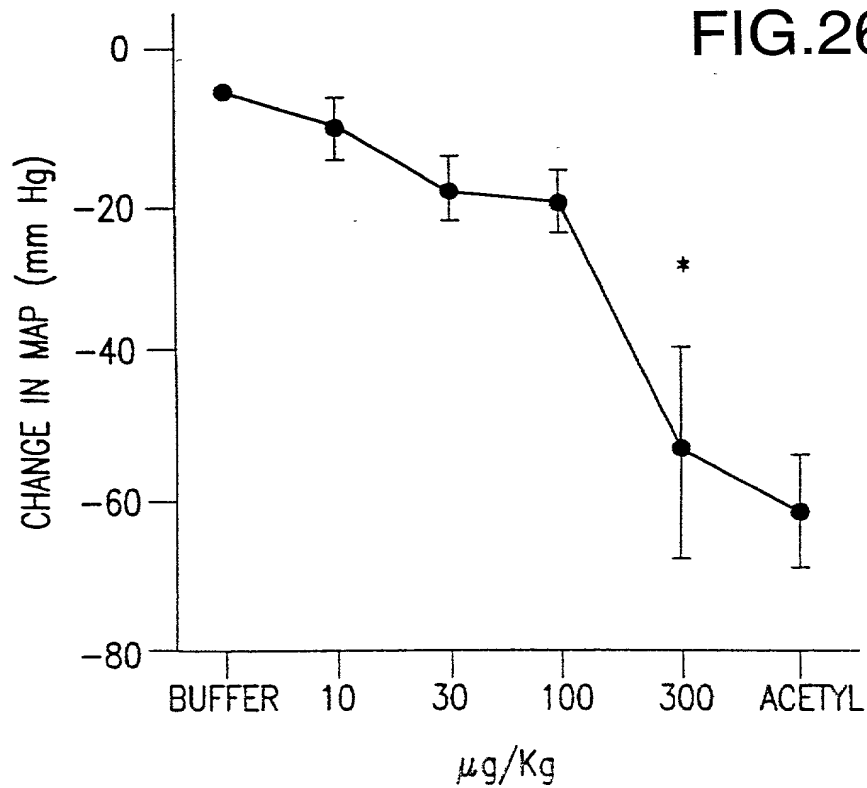


FIG.26D



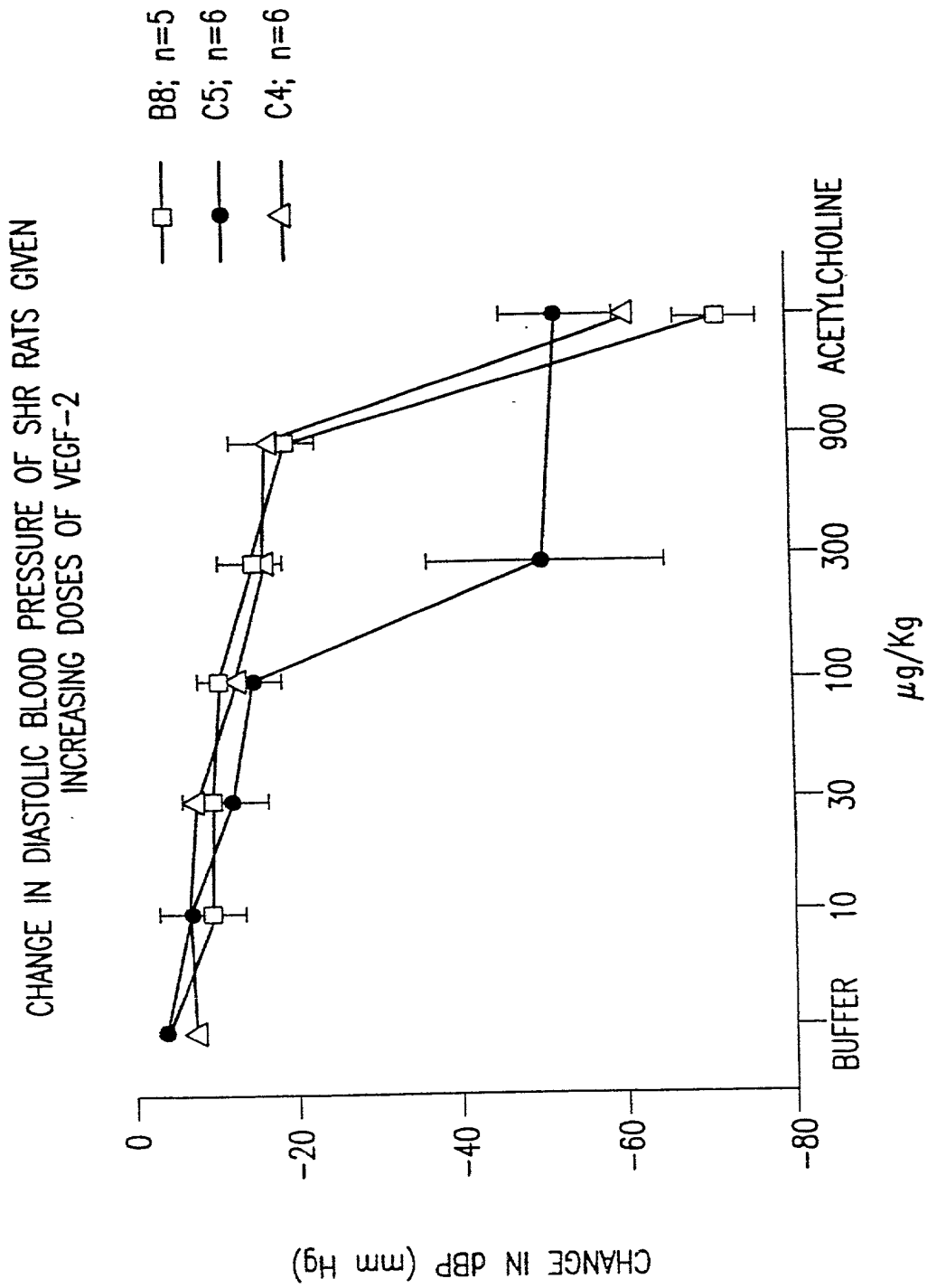


FIG.26E

THE EFFECT OF INCREASING DOSES OF VEGF-2 ON THE
MEAN ARTERIAL PRESSURE (MAP) OF SHR RATS

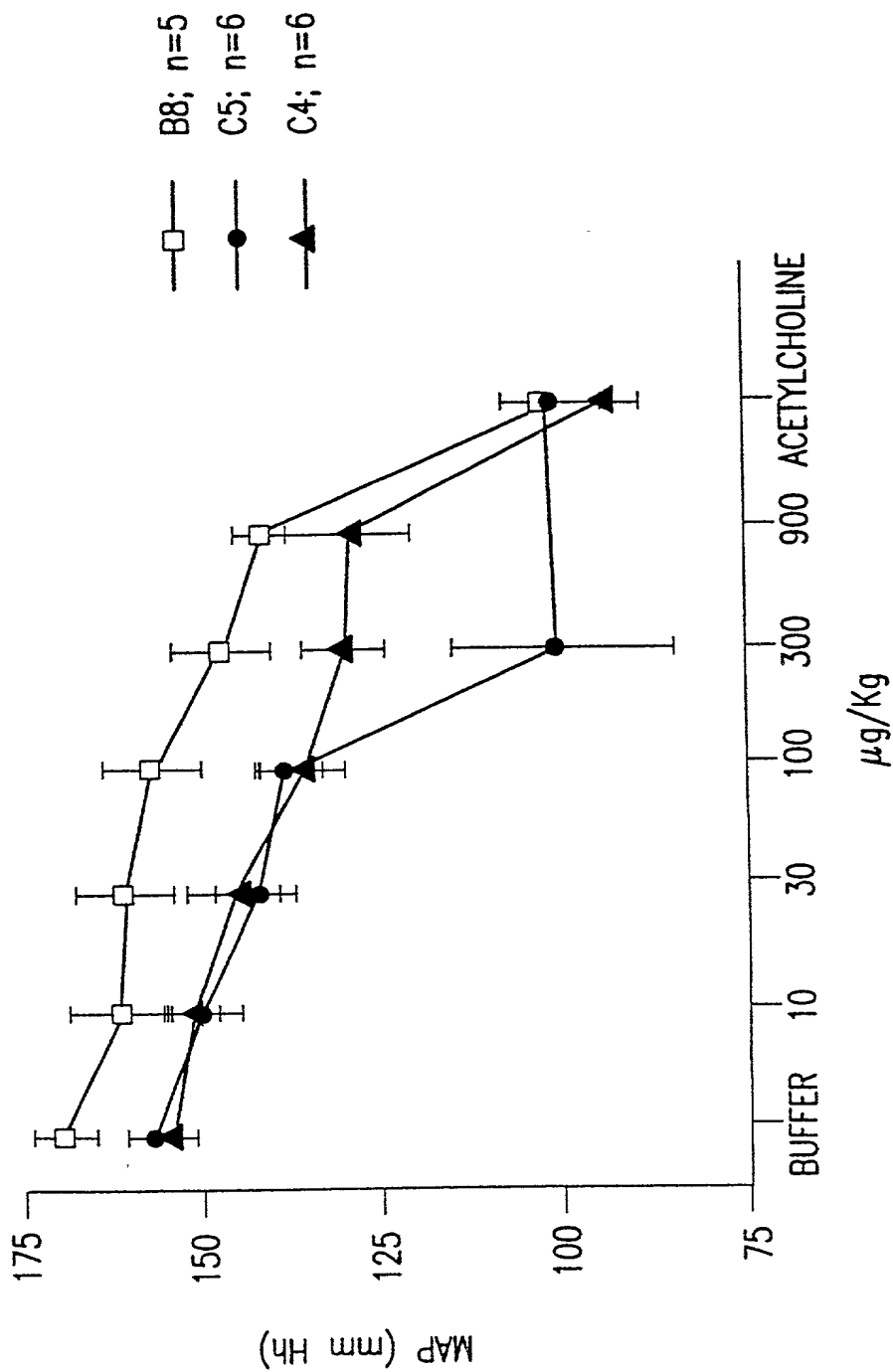


FIG.26F

THE EFFECT OF VEGF-2 ON THE DIASTOLIC BLOOD PRESSURE OF SHR RATS

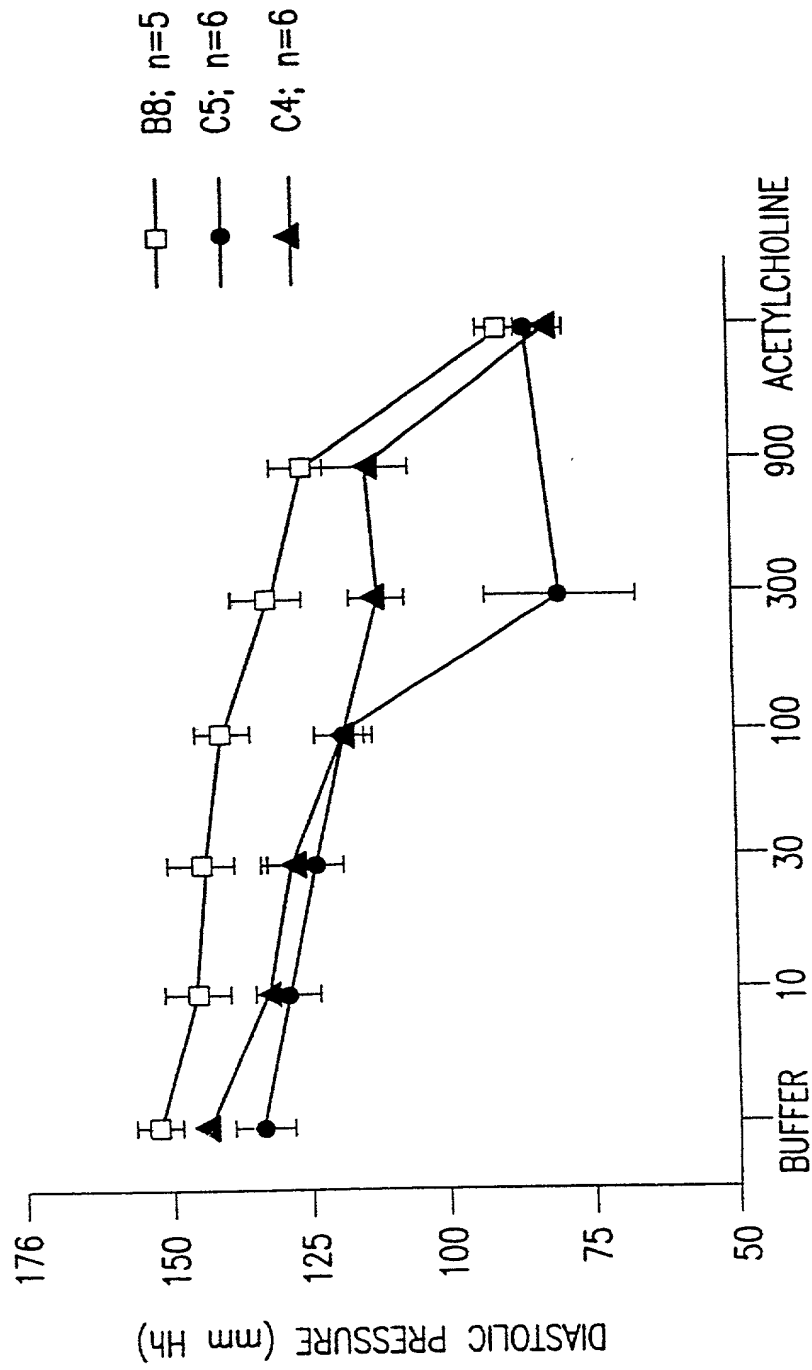


FIG.26G

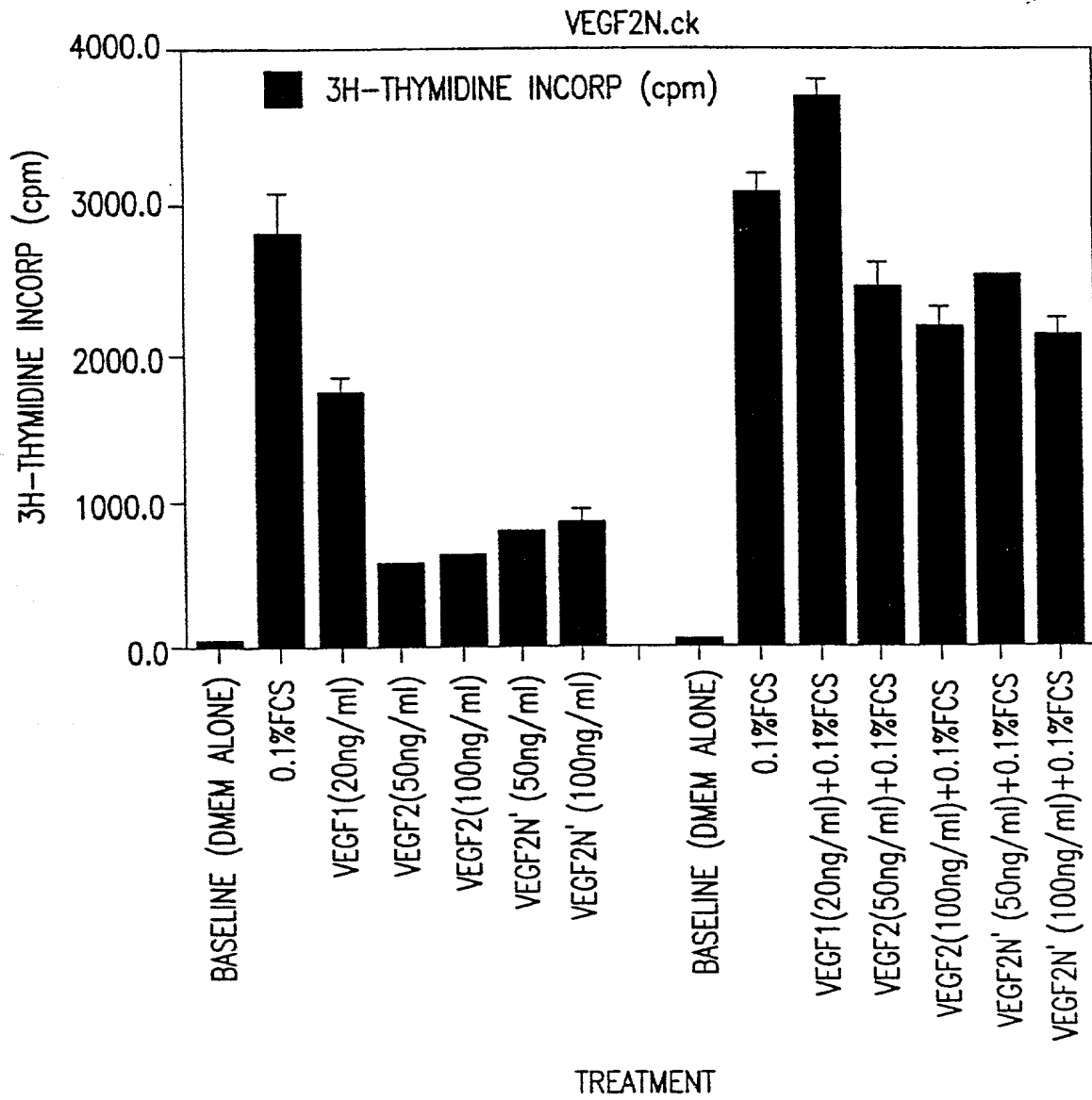


FIG.27

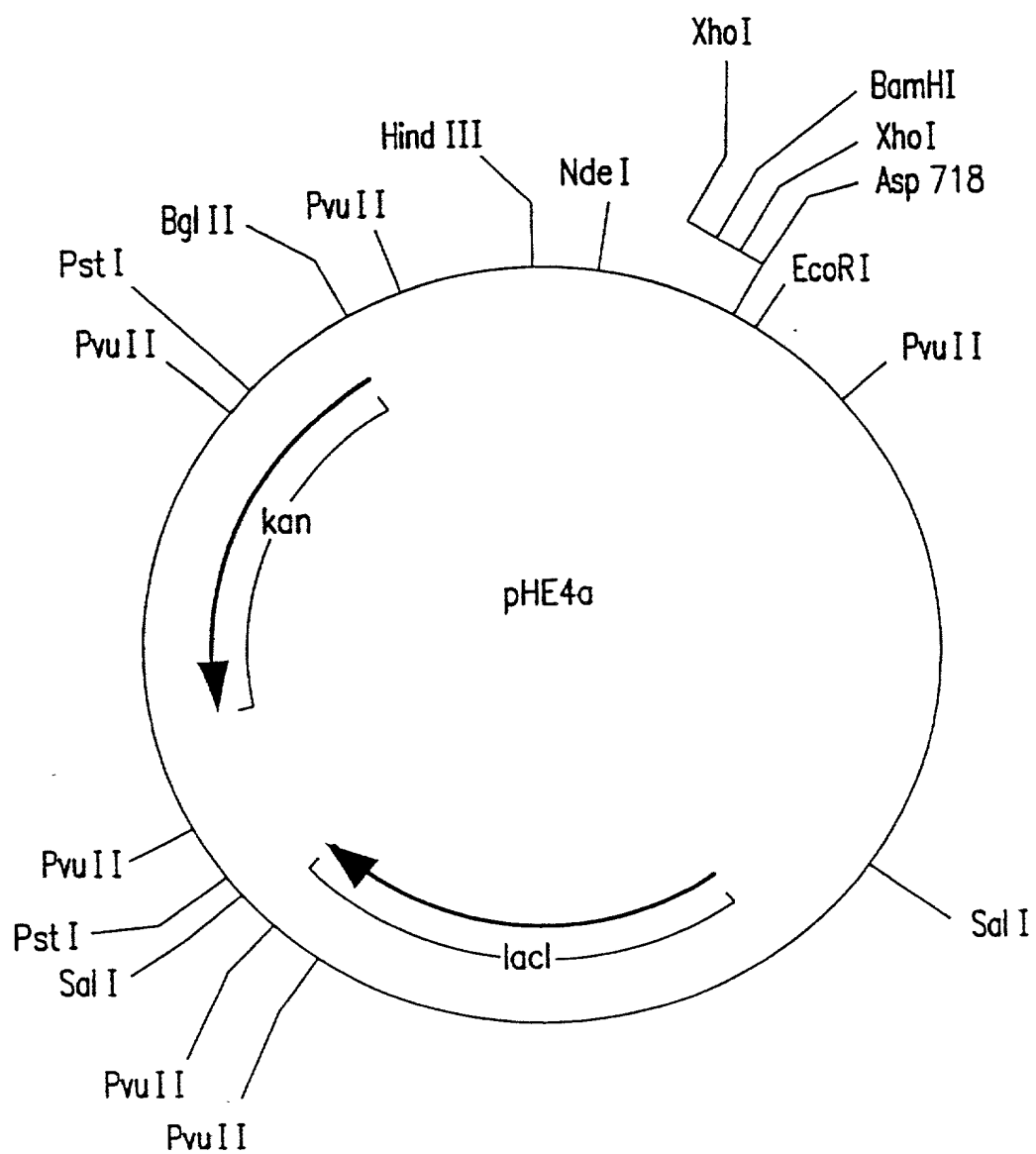


FIG.28

OPERATOR 1

-35

I AAGCTTAAAACTGCAAAATAGT T T G A C T T G T G A G C C G A T A A C A A T

-10

OPERATOR 2

50 T A A G A T G T A C C C A A T T G T G A G C C G A T A A C A A T T T C A C A C A T T A A

S/D

94 A G A G G A G A A A T T A C A T A T G

FIG.29